

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 5, 2003, 17:55:23 ; Search time 80 seconds
(without alignments)
426.378 Million call updates/sec

Title: US-09-936-680-2

Perfect score: 1124
Sequence: 1 MFANRUFFLASULVYWS.....SDVLAISFENKSNVFEV 215

Scoring table: BLOSUM62

Gap: 10.0 , Gapext: 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Maximum DB seq length: 2000000000

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum DB seq length: 2000000000

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24: /SIDSI1/gcgdata/geneseq/geneseq-emb/AA2003.DAT*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	1124	100.0	215	21 AAB36002 Human beta3 subunit
2	1124	100.0	215	22 AAB8206 Human beta3 subunit
3	1124	100.0	215	23 AAB95489 Human signal trans
4	1105	98.3	215	24 AAB50243 Human beta3 subunit
5	1105	98.3	215	25 AAB50243 Rat sodium channel
6	1024	91.1	195	22 AAB79212 Human protein SEQ
7	986	87.7	191	22 AAB50245 Rat sodium channel
8	943	83.6	191	22 AAB50245 Novel human diapo
9	843	73.6	159	21 AAB30200 Human beta3 subunit

10	832	74.0	159	21 AAB30201 Rat beta3 subunit
11	694	61.7	1176	22 AAB22576 Novel human diapo
12	477	42.4	218	22 AAB50260 Rabbit sodium chan
13	472	42.0	218	21 AAB36031 Rat beta3 subunit
14	472	42.0	218	21 AAB36031 Rat beta3 subunit
15	472	42.0	218	21 AAB36031 Rat beta3 subunit
16	408.5	36.3	206	22 AAB82775 Human voltage-gate
17	258.5	23.0	268	23 AAB22575 Novel human diapo
18	246	21.9	268	23 AAB18634 Human beta3a sodiu
19	246	21.9	272	22 AAB23370 Rat sodium channel
20	234	20.8	74	22 AAB31698 Human voltage-gate
21	234	20.8	74	22 AAB31698 Human voltage-gate
22	227	19.4	39	21 AAB36015 Human beta3 subunit
23	227	19.4	39	21 AAB36015 Human beta3 subunit
24	165	14.7	34	21 AAB36029 Human beta3 subunit
25	163.5	14.5	258	23 AAB53696 Human myelin prote
26	161	14.3	34	21 AAB36034 Human beta3 subunit
27	161	14.3	34	21 AAB36034 Human beta3 subunit
28	160.5	14.3	235	22 AAB60121 Human transport pr
29	160.5	14.3	235	23 AAB3710 Human PRO7425 prot
30	160.5	14.3	235	23 AAB3710 Human PRO7425 prot
31	159	14.3	235	23 AAB3710 Human PRO7425 prot
32	149	13.3	246	23 AAB94567 Mouse major paritph
33	147	13.1	215	20 AAV41673 Human channel-rela
34	147	13.1	215	21 AAB33448 Human PRO1192 prot
35	147	13.1	215	21 AAB33448 Human PRO1192 prot
36	147	13.1	215	21 AAB33448 Human PRO1192 prot
37	147	13.1	215	22 AAB62575 Human PRO1192 (UNQ
38	147	13.1	215	23 AAB95515 Human angiogenesis
39	147	13.1	215	23 AAB84909 Human PRO1192 (UNQ
40	147	13.1	215	23 AAB84909 Human PRO1192 (UNQ
41	147	13.1	215	24 AAB6813 Human PRO polypept
42	147	13.1	215	24 AAB6813 Human secreted/tra
43	147	13.1	215	24 AAB59684 Novel secreted and
44	147	13.1	215	24 AAB59684 Novel secreted and
45	147	13.1	215	24 AAB59684 Human secreted/tra

ALIGNMENTS

RESULT 1
AAB36002 standard; protein, 215 AA.

XX AAB36002;
XX AAB36002 (first entry)
XX 15-FEB-2001 (first entry)
XX Human beta3 subunit.

XX Human; beta sub-unit; beta3; analgesic; anticonvulsant;
XX cerebroprotective; vasotropic; cardiac; motropic; cytostatic;
XX dermatological; gene therapy; voltage-gated sodium channel; pain;
XX epilepsy; stroke; ischemia; heart disease; Jacobson Syndrome;
XX Huntington's disease; Angelman, phenylketonuria,
XX Charcot Marie Tooth disease.

XX Homo sapiens.

XX WO20060367-A1.

XX 26-OCT-2000.

XX 24-FEB-2000; 2000WO-SP01783.

XX 15-APR-1999; 99US-0129473.

XX (WARR) WARNER LAMBERT CO.

XX (UYCA) UNIV CAMBRIDGE TECH SERVICES LTD.

XX Cox P, Dixon A, Jackson A, Morgan K;

DR WPI; 2000-665241/64.
 DR N-FSD0; AAC67837.
 XX Novel nucleic acids encoding a beta-3 subunit from a voltage-gated
 FT sodium channel, and their corresponding polypeptides, useful for
 FT detecting and treating sodium channel-associated conditions, e.g. pain,
 FT epilepsy and stroke -

PS Claim 34; Fig 4; 8pp; English.

XX The present sequence is given in the claims of a specification
 CC relating to a novel family of beta sub-unit proteins from a
 CC voltage-gated sodium channel. Human and rat beta sub-units, which
 CC have been collectively identified as beta3, have been isolated.
 CC The present invention provides a novel beta3-like subunit useful for
 CC detecting and treating sodium channel-associated conditions, e.g. pain,
 CC epilepsy and stroke -

XX The invention provides a novel beta3-like sub-unit for voltage-gated
 CC sodium channels. The novel beta3-like subunit is useful for
 CC channel (SNS) subunit. The novel beta3-like subunit is useful for
 CC producing a therapeutic agent which is useful treating pain in a patient.
 CC The subunit can be expressed by standard recombinant methodology. The
 CC present sequence represents a human novel sodium channel beta3-like
 CC subunit.

XX Sequence 215 AA;

Query Match 100.0%; Score 1124; DB 21; Length 215;
 Best Local Similarity 100.0%; Pred. No. 1.4e-97;
 Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPANRFLPLASLILVYWSVCFVCPVSETEAVQGNPKMKLCISCKMREVEATTV 60
 DB 1 MPANRFLPLASLILVYWSVCFVCPVSETEAVQGNPKMKLCISCKMREVEATTV 60
 QY 61 EWPYRPGSGKPLIYETRNHGQVESPFCQRLQNGSKDQVSIYLVNTLNSGLYTC 120
 DB 61 EWPYRPGSGKPLIYETRNHGQVESPFCQRLQNGSKDQVSIYLVNTLNSGLYTC 120
 QY 121 WVSREFEFAHPPVATLILPVYTRKAGEDFTSVSEIMVILLVFLTLLMIEMVYC 180
 DB 121 WVSREFEFAHPPVATLILPVYTRKAGEDFTSVSEIMVILLVFLTLLMIEMVYC 180
 QY 181 YRKSVAEAAQNASDYLAIPTSENKENSANPVVEE 215
 DB 181 YRKSVAEAAQNASDYLAIPTSENKENSANPVVEE 215

RESULT 2

AAB85206
 ID AAB85206 standard; Protein; 215 AA.
 XX
 AC AAB85206;
 XX
 XT 07-SEP-2001 (first entry)
 XX Human novel sodium channel beta3-like subunit.
 DE Human novel sodium channel beta3-like subunit.
 XX Sodium channel; sensory neuron specific channel, beta3-like subunit;
 XX SNS; thoracic; pain management.

OS Homo sapiens.

XX Key Location/Qualifiers
 FT Domain 38..122
 FT Domain /note="immunoglobulin domain"
 FT Domain 157..176
 FT Domain /note="transmembrane domain"

XX W0200344293.A2.

XX 21-JUN-2001.

XX 14-DEC-2000; 200QWO-GB04802.

XX 17-DEC-1999; 99GB-0029970.

XX

XX (GLAXO) GLAXO GROUP LTD.

XX Plumpdon M, Powell AJ, Sansau P;

XX WPI; 2001-398129/42.
 XX N-FSD0; AAF84116.

XX Novel sub-unit for voltage-gated sodium channel proteins for producing
 FT agents useful for treating pain -

PS Claim 1; Fig 2; 3pp; English.

XX The invention provides a novel beta3-like sub-unit for voltage-gated
 CC sodium channels. The novel beta3-like subunit is useful for
 CC channel (SNS) subunit. The novel beta3-like subunit is useful for
 CC producing a therapeutic agent which is useful treating pain in a patient.
 CC The subunit can be expressed by standard recombinant methodology. The
 CC present sequence represents a human novel sodium channel beta3-like
 CC subunit.

XX Sequence 215 AA;

Query Match 100.0%; Score 1124; DB 22; Length 215;
 Best Local Similarity 100.0%; Pred. No. 1.4e-97;
 Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPANRFLPLASLILVYWSVCFVCPVSETEAVQGNPKMKLCISCKMREVEATTV 60
 DB 1 MPANRFLPLASLILVYWSVCFVCPVSETEAVQGNPKMKLCISCKMREVEATTV 60
 QY 61 EWPYRPGSGKPLIYETRNHGQVESPFCQRLQNGSKDQVSIYLVNTLNSGLYTC 120
 DB 61 EWPYRPGSGKPLIYETRNHGQVESPFCQRLQNGSKDQVSIYLVNTLNSGLYTC 120
 QY 121 WVSREFEFAHPPVATLILPVYTRKAGEDFTSVSEIMVILLVFLTLLMIEMVYC 180
 DB 121 WVSREFEFAHPPVATLILPVYTRKAGEDFTSVSEIMVILLVFLTLLMIEMVYC 180
 QY 181 YRKSVAEAAQNASDYLAIPTSENKENSANPVVEE 215
 DB 181 YRKSVAEAAQNASDYLAIPTSENKENSANPVVEE 215

RESULT 3

AAB85689
 ID AAB85689 standard; Protein; 215 AA.
 XX
 AC AAB85689;
 XX

XX 30-APR-2002 (first entry)

XX Human signal transduction protein clone amy2_2f18.

XX Human; foetal brain; foetal kidney; melanoma; testis; amygdala;
 XX gene therapy.
 OS Homo sapiens.

XX W0200199454.A2.

XX 27-DEC-2001.

XX 25-APR-2001; 2001WO-1802050.

XX 25-APR-2000; 2000US-199380P.

XX (GEO) - GERMAN HUMAN GENOME PROJECT.

XX Wilmann S;

XX WPI; 2002-055860/07.

XX N-FSD0; ABA93727.


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OS Homo sapiens.
XX MW0200063367-A1.
XX PD 26-OCT-2000.
XX PF 24-FEB-2000; 2000WO-EF01783.
XX PA (WARN ) WARNER LAMBERT CO.
XX PA (UTCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
XX PT Cox P, Dixon A, Jackson A, Morgan K;
XX WPI; 2000-665241/64.
XX DR Novel nucleic acids encoding a beta-3 subunit from a voltage-gated
XX PT sodium channel, and their corresponding polypeptides, useful for
XX PT detecting and treating sodium channel-associated conditions, e.g. pain,
XX PT epilepsy and stroke.
XX PS Claim 36; Page 76; 88pp; English.
XX CC The present sequence is given in the claims of a specification
XX CC relating to a novel family of beta sub-unit proteins from a
XX CC voltage-gated sodium channel. Human and rat beta sub-units, which
XX CC have been collectively identified as beta3, have been isolated.
XX CC The polynucleotides and polypeptides are useful for screening for
XX CC agonists and antagonists of sodium channels. The agonists, antagonists,
XX CC or conditions associated with voltage-gated sodium channels, e.g.
XX CC pain, epilepsy, stroke, ischaemia, heart disease, Jacobson Syndrome, Familial
XX CC Nonchromaffin Paraganglioma, Phenylketonuria and Charcot Marie Tooth
XX CC disease.
XX SQ Sequence 159 AA;
XX Query Match 74.0%; Score 832; DB 21; Length 159;
XX Best Local Similarity 98.7%; Pred. No. 2.6e-70;
XX Matches 157; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MPANRLLPFLASLVLTVVSCVPCVVPSTETAVQNPMKLCISCKRREVAITTV 60
DB 1 MPANRLLPFLASLVLTVVSCVPCVVPSTETAVQNPMKLCISCKRREVAITTV 60
QY 61 EMFVPEEGSGDPLIFVFNHGVHSPQRIQWNSKDLQVSVITVAVNLNSGLTVC 120
DB 61 EMFVPEEGSGDPLIFVFNHGVHSPQRIQWNSKDLQVSVITVAVNLNSGLTVC 120
QY 121 NVSRFEFEARHFFVATLLIPVRYTEAGDFTSVSE 159
DB 121 NVSRFEFEARHFFVATLLIPVRYTEAGDFTSVSE 159
RESULT 11
AB022576
ID AB022576 standard; Protein; 1176 AA.
XX AC AB022576;
XX DT 18-FEB-2002 (first entry)
XX DE Rat beta3 subunit peptide, SEQ ID NO: 23.
XX RT; beta sub-unit; beta3; analgesic; anticonvulsant;
XX KW cerebroprotective; vasotropic; cardiant; nontopic; cyrostatic;
XX KW dermatological; gene therapy; voltage-gated sodium channel; pain;
XX KW epilepsy; atroce; ischaemia; heart disease; Jacobson Syndrome;
XX KW Charcot Marie Tooth disease.
XX OS Rattus sp.
XX
XX Query Match 74.0%; Score 832; DB 21; Length 159;
XX Best Local Similarity 100.0%; Pred. No. 2.6e-71;
XX Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPANRLLPFLASLVLTVVSCVPCVVPSTETAVQNPMKLCISCKRREVAITTV 60
DB 1 MPANRLLPFLASLVLTVVSCVPCVVPSTETAVQNPMKLCISCKRREVAITTV 60
QY 61 EMFVPEEGSGDPLIFVFNHGVHSPQRIQWNSKDLQVSVITVAVNLNSGLTVC 120
DB 61 EMFVPEEGSGDPLIFVFNHGVHSPQRIQWNSKDLQVSVITVAVNLNSGLTVC 120
QY 121 NVSRFEFEARHFFVATLLIPVRYTEAGDFTSVSE 159
DB 121 NVSRFEFEARHFFVATLLIPVRYTEAGDFTSVSE 159
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AB035021
ID AAB35021 standard; Protein; 159 AA.
XX AC AAB35021;
XX DT 15-FEB-2001 (first entry)
XX DE Rat beta3 subunit peptide, SEQ ID NO: 23.
XX RT; beta sub-unit; beta3; analgesic; anticonvulsant;
XX KW cerebroprotective; vasotropic; cardiant; nontopic; cyrostatic;
XX KW dermatological; gene therapy; voltage-gated sodium channel; pain;
XX KW epilepsy; atroce; ischaemia; heart disease; Jacobson Syndrome;
XX KW Charcot Marie Tooth disease.
XX OS Rattus sp.

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PN WO20063367-A1.
 XX 26-OCT-2000.
 XX 24-FEB-2001; 2006WO-SP01783.
 XX 15-APR-1999; 99US-0129473.
 XX (WASN) WARNER LAMBERT CO.
 PA (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
 PT Cox P, Dixon A, Jackson A, Morgan K;
 XX WPI; 2000-66541/64.
 DR Novel nucleic acids encoding a beta-3 subunit from a voltage-gated
 PT sodium channel, and their corresponding polypeptides, useful for
 PT detecting and treating sodium channel-associated conditions, e.g. pain,
 PT epilepsy and stroke -
 XX Disclosure; Fig 4; 8pp; English.
 XX The present sequence is given in a specification relating to a novel
 CC human and rat beta sub-units, which have been collectively identified
 CC as beta3. The polynucleotides and polypeptides are
 CC useful for screening for agonists and antagonists of sodium channels.
 CC The polynucleotides and polypeptides are also used
 CC in the diagnosis and treatment of diseases or conditions associated with
 CC voltage-gated sodium channels, e.g. pain, epilepsy, stroke, ischaemia,
 CC heart disease, Jacobson Syndrome, Familial Nonchromaffin
 CC paraganglioma, Phenylketonuria and Charcot Marie Tooth disease.
 XX Sequence 218 AA;
 SQ
 Query Match 42.04; Score 472; DB 21; Length 218;
 Best Local Similarity 43.13; Pred No. 2,7e-36;
 Matches 105; Conservative 33; Mismatches 68; Indels 8; Gaps 5;
 QY 10 LAGULVYGVSVCTPVGVVSTETAVGVNPKWGLCTSCMRDEHVAIVTVVSTVREGG 69
 DB 5 LAUVGVAVVSSAGGCVGVSTETAVGVNPKWGLCTSCMRDEHVAIVTVVSTVREGG 64
 QY 70 VQPL-IYEVNKHQVQESP--PQSLQWNGS--KVLQGVSTVTVNVLNLSGLTVQVNS 123
 DB 65 EFVFKLYEVNVLQEDREDFGVVNGSRTGLQSLIFITVTVNNSGDYCHVY 124
 QY 124 REFEHAMPFPVFTVTLPLAVTVBAGSFTSVSGHETHTLTVPLTGLLIMHYCVVK 183
 DB 125 RLKFDNFBHTSVVKKHLEVDVNDKRMASVSEIMVVLVILTVLVAEMVYCYK 184
 QY 184 VSKA-EEAAGNSGVHAIPEENKVN-SANVPEE 215
 DB 185 IAAATEAAGNSAEVLATSEKNCCTGVAAE 218
 RESULT 14
 AAB62326
 ID AAB62326 standard; Protein; 218 AA.
 XX AAB62326;
 XX 29-JUN-2001 (first entry)
 DT Rat sodium channel beta-1 subunit amino acid sequence.
 XX sodium channel; modulator; sodium channel beta-1A subunit; pain; rat;
 XX sodium channel beta-1 subunit; analgesic; neuroprotective.
 XX Rattus sp.
 XX MO200123570-A2.
 PN
 PD 05-APR-2001.
 XX 29-SEP-2000; 2000WO-US27034.
 XX 30-SEP-1999; 99US-0156837.
 XX (ORTH) ORTHO-McNEIL PHARM INC.
 XX D'Andrea M, Rogers ME;
 FI WPI; 2001-281683/29.
 XX Screening for sodium channel activity modulators, used to decrease
 PT neuropathic pain, comprises contacting a candidate compound with a cell
 PT expressing the channel -
 XX Examples; Fig 1B; 124pp; English.
 XX The invention relates to a method of screening for a modulator of sodium
 CC cell co-expressing a sodium channel beta-1A subunit with a sodium channel
 CC alpha subunit, and determining the effect of the candidate modulator on
 CC the sodium channel function in the cell. The method is useful for
 CC screening for compounds that modulate sodium channel activity. The method
 CC decreased beta 1A subunit expression. The modulators can be used to
 CC decrease neuropathic pain, and to decrease the number of febrile seizures
 CC in an individual. The present sequence represents a rat sodium channel
 CC beta-1 subunit, used in homology studies with the beta-1A subunit.
 XX Sequence 218 AA;
 SQ
 Query Match 43.09; Score 472; DB 22; Length 218;
 Best Local Similarity 43.13; Pred No. 2,7e-36;
 Matches 105; Conservative 33; Mismatches 68; Indels 8; Gaps 5;
 QY 10 LAGULVYGVSVCTPVGVVSTETAVGVNPKWGLCTSCMRDEHVAIVTVVSTVREGG 69
 DB 5 LAUVGVAVVSSAGGCVGVSTETAVGVNPKWGLCTSCMRDEHVAIVTVVSTVREGG 64
 QY 70 VQPL-IYEVNKHQVQESP--PQSLQWNGS--KVLQGVSTVTVNVLNLSGLTVQVNS 123
 DB 65 EFVFKLYEVNVLQEDREDFGVVNGSRTGLQSLIFITVTVNNSGDYCHVY 124
 QY 124 REFEHAMPFPVFTVTLPLAVTVBAGSFTSVSGHETHTLTVPLTGLLIMHYCVVK 183
 DB 125 RLKFDNFBHTSVVKKHLEVDVNDKRMASVSEIMVVLVILTVLVAEMVYCYK 184
 QY 184 VSKA-EEAAGNSGVHAIPEENKVN-SANVPEE 215
 DB 185 IAAATEAAGNSAEVLATSEKNCCTGVAAE 218
 RESULT 15
 AAB82771
 ID AAB82771 standard; Protein; 218 AA.
 XX AAB82771;
 XX 18-MAR-2003 (first entry)
 DT Human voltage-gated sodium channel mutant beta-1 subunit.
 XX Sodium channel; mutation; epilepsy; anticonvulsant; mutant; human;
 XX SC18; gene; de.
 XX Homo sapiens.
 XX MO200290532-A1.
 XX 14-NOV-2002.
 XX 09-MAY-2002; 2002WO-AU00581.
 XX

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 5, 2003, 22:59:23 ; Search time 44 seconds
(44000 alignments)
469,515 Million cell updates/sec

Title: US-09-936-680-2

Perfect score: 112.21 (100% alignment)
Sequence: 1 WPAWNPFLASLVLVWVS.....SDVLAISWENASNPYVER 215

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96166862 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 10%

Listing first 45 summaries

Database :

1: p11.*

2: p12.*

3: p13.*

4: p14.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Length	DB	ID	Description
1	477	42.4	218	2	JC4788	sodium channel protein
2	472	42.0	218	2	JC4787	sodium channel protein
3	470	41.8	218	2	JC4786	sodium channel protein
4	470	41.8	218	2	JC4785	sodium channel protein
5	163.5	14.5	248	1	NP870	myelin P0 protein
6	163.5	14.5	248	1	JH0252	myelin P0 protein
7	163.5	14.5	251	2	J38053	myelin P0 protein
8	154.5	13.7	247	1	A44622	myelin P0 protein
9	144.5	12.9	246	1	A12399	myelin P0 protein
10	140.5	12.5	249	1	A61087	myelin P0 glycoprotein
11	137.5	12.0	246	1	A61087	myelin P0 glycoprotein
12	137.5	12.0	246	1	A61087	myelin P0 glycoprotein
13	111.5	9.9	820	2	S17295	fibroblast growth
14	111.5	9.9	821	1	TWMSBK	protein-tyrosine
15	110.5	9.8	482	1	B6102P	protein-tyrosine
16	107.5	9.5	800	2	A48391	heparin-binding
17	107.5	9.5	800	2	A48391	heparin-binding
18	107.5	9.5	801	2	I53563	fibroblast growth
19	103.5	9.2	129	2	S57884	T cell receptor
20	103.5	9.2	129	2	S57884	T cell receptor
21	103.5	9.2	372	2	C39171	IG V-region-like B
22	101.5	9.0	806	2	A35663	protein-tyrosine k
23	100.5	8.9	790	2	S42053	fibroblast growth
24	100.5	8.9	790	2	S42053	fibroblast growth
25	99.5	8.9	131	2	B10577	IG kappa chain pre
26	99.5	8.9	131	2	P01078	IG kappa chain pre
27	99.5	8.9	821	1	TWMSBK	protein-tyrosine
28	99.5	8.9	821	1	TWMSBK	protein-tyrosine
29	98.5	8.8	133	2	D44304	IG kappa chain pre

ALIGNMENTS

RESULT 1

JC4788

sodium channel protein beta chain - rabbit

C-Species: *Oryzotegus cuniculus* (domestic rabbit)

C-Date: 10-Nov-1999 #sequence_revision 16-Aug-1996 #ext_change 05-Nov-1999

R-Builder: S.M.; Howe, J.R.

Gene 170, 285-286, 1996

A-Title: Cloning of the cDNA encoding the sodium channel beta subunit from rabbit.

A-Accession: J04788

A-Molecule type: mRNA

A-Residue: 1-218

C-Comment: This protein is composed of a large alpha-chain and two small beta-chains and a beta-2 subunit.

C-Keywords: glycoprotein; membrane protein; muscle; transmembrane protein

C-Keywords: P161182/Domain; transmembrane status predicted <TM>

F193,110,114,135/Binding site; carbohydrate (Aam) (covalent) #status predicted

Query Match 42.4%; Score 477; DB 2; Length 218;

Best Local Similarity 49.5%; Pred. No. 2, 58-33;

Matches 106; Conservative 32; Mismatches 68; Indels 8; Gaps 5;

QY 10 LASVLYLVWVCPVCPVSTAVQCNPKRCISCKRBEVATVWVFYRGG 69

DB 5 LAPVGAALVSSAGCQVSTSTAVTQMTFKLCISCKRSETTATFTMTFQKT 64

QY 70 KDFU-LVYVSHQVSESP--FGSLDQWKS--KLDQVSTLVANLGLSTQVNS 123

DB 65 BEPVLAYNEVLQEDERFGVYVSGRTQDQSLSTFTVTVHSGDQCHVY 124

QY 124 BEPVLAYNEVLQEDERFGVYVSGRTQDQSLSTFTVTVHSGDQCHVY 183

DB 125 RLSPENYTSVVKHLEVDQANRDMASVSEIMTVLTVTVNVAWVYCKK 184

QY 184 VSDQ-EDAAQWSDVLAISENKN-SNPYVER 215

DB 185 IAAATEAAQWSDVLAISENKNCTQVAE 218

RESULT 2

A42737

sodium channel beta 1 subunit - rat

C-Species: *Stomoxys calcitrans* (house fly)

C-Date: 10-Nov-1999 #sequence_revision 10-Nov-1994 #ext_change 05-Nov-1999

R-Builder: S.M.; Howe, J.R.

A-Accession: A42737

A-Molecule type: mRNA

A-Residue: 1-218

C-Comment: This protein is composed of a large alpha-chain and two small beta-chains and a beta-2 subunit.

C-Keywords: glycoprotein; membrane protein; muscle; transmembrane protein

C-Keywords: P161182/Domain; transmembrane status predicted <TM>

F193,110,114,135/Binding site; carbohydrate (Aam) (covalent) #status predicted

Query Match 42.4%; Score 477; DB 2; Length 218;

Best Local Similarity 49.5%; Pred. No. 2, 58-33;

Matches 106; Conservative 32; Mismatches 68; Indels 8; Gaps 5;

A:Reference number: A42737; MUID:92271807; PMID:1375395

A:Accession: M42737

C:Species: Homo sapiens (man)

C:Accession: A5734; revision 18-Aug-1995 #text_change 08-Oct-1999

C:Keywords: voltage-gated, beta-1 chain precursor - human

A:Molecule type: nucleic acid; protein

A:Residues: 1-218 <150>

A:Cross-references: GB:M91808; PID:AA48513.1; PID:g506865

A:Note: sequence extracted from NCBI backbone (NCBI:103298)

C:Keywords: transmembrane protein

Query Match 42.08; Score 472; DB 2; Length 218;

Best Local Similarity 49.18; Pred. No. 6.7e-33;

Matches 105; Conservative 33; Mismatches 68; Indels 8; Gaps 5;

QY 10 LASHLLVWVSCVPCVVESEVETAVGNGWMLGICSGKQSEEVATVVFVYRPEGG 69

DB 5 LALVGGALVSSAGGCGVEVSEVATVGTFTKLCICGGRSEETATFTFTFRQGT 64

QY 70 KDEFLVYVNGHQVESP--FQGLRQNGS--KDLQDSITVLVNLSDGLGTVNS 123

DB 65 EEFVKLLVENVGLDEDEPERGVVNGSGRTGLDLSIFITVYHNSGVDECHY 124

QY 124 REFFEMARVFKTRLLDPTVETAGDEPTFVSQVSEVMTKLLAFVTLVHMYCYRK 183

DB 125 RLFPFNTYHNTSVVKKHGVQDKAMNATVSSIMVLLVLTWVAEMVICYRK 184

QY 184 VSKA-REAGASVADSVLAIDSNKSN-SAVDPE 215

DB 185 IMAATETAAGNSAYLAITSSEKNGCTGVAAE 218

RESULT 3

A:Molecule type: DNA

A:Accession: A5734

A:Title: sodium channel, voltage-gated, beta-1 chain precursor - human

A:Residues: 1-248 <150>

A:Accession: A22822

A:Title: isolation and sequence of a cDNA encoding the major structural protein of per

A:Reference number: A5734; MUID:9514893; PMID:7851891

A:Accession: A5734

A:Molecule type: mRNA

A:Accession: A5734

A:Title: sodium channel, voltage-gated, beta-1 chain precursor - human

A:Residues: 1-248 <150>

A:Accession: A22822

A:Title: isolation and sequence of a cDNA encoding the major structural protein of per

A:Reference number: A5734; MUID:9514893; PMID:7851891

A:Accession: A5734

A:Molecule type: mRNA

A:Accession: A5734

A:Title: sodium channel, voltage-gated, beta-1 chain precursor - human

A:Residues: 1-248 <150>

A:Accession: A22822

A:Title: isolation and sequence of a cDNA encoding the major structural protein of per

A:Reference number: A5734; MUID:9514893; PMID:7851891

A:Accession: A5734

A:Molecule type: mRNA

A:Accession: A5734

A:Title: sodium channel, voltage-gated, beta-1 chain precursor - human

A:Residues: 1-248 <150>

A:Accession: A22822

A:Title: isolation and sequence of a cDNA encoding the major structural protein of per

A:Reference number: A5734; MUID:9514893; PMID:7851891

A:Accession: A5734

A:Molecule type: mRNA

A:Accession: A5734

A:Title: sodium channel, voltage-gated, beta-1 chain precursor - human

A:Residues: 1-248 <150>

A:Accession: A22822

A:Title: isolation and sequence of a cDNA encoding the major structural protein of per

A:Reference number: A5734; MUID:9514893; PMID:7851891

A:Accession: A5734

A:Molecule type: mRNA

A:Accession: A5734

A:Title: sodium channel, voltage-gated, beta-1 chain precursor - human

A:Residues: 1-248 <150>

A:Accession: A22822

A:Title: isolation and sequence of a cDNA encoding the major structural protein of per

A:Reference number: A5734; MUID:9514893; PMID:7851891

A:Accession: A5734

A:Molecule type: mRNA

A:Accession: A5734

A:Title: sodium channel, voltage-gated, beta-1 chain precursor - human

A:Residues: 1-248 <150>

A:Accession: A22822

A:Title: isolation and sequence of a cDNA encoding the major structural protein of per

A:Reference number: A5734; MUID:9514893; PMID:7851891

A:Accession: A5734

A:Molecule type: mRNA

A:Accession: A5734

Match 106; Conservative 31; Mismatches 69; Indels 8; Gaps 5;

QY 10 LASHLLVWVSCVPCVVESEVETAVGNGWMLGICSGKQSEEVATVVFVYRPEGG 69

DB 5 LALVGGALVSSAGGCGVEVSEVATVGTFTKLCICGGRSEETATFTFTFRQGT 64

QY 70 KDEFLVYVNGHQVESP--FQGLRQNGS--KDLQDSITVLVNLSDGLGTVNS 123

DB 65 EEFVKLLVENVGLDEDEPERGVVNGSGRTGLDLSIFITVYHNSGVDECHY 124

QY 124 REFFEMARVFKTRLLDPTVETAGDEPTFVSQVSEVMTKLLAFVTLVHMYCYRK 183

DB 125 RLFPFNTYHNTSVVKKHGVQDKAMNATVSSIMVLLVLTWVAEMVICYRK 184

QY 184 VSKA-REAGASVADSVLAIDSNKSN-SAVDPE 215

DB 185 IMAATETAAGNSAYLAITSSEKNGCTGVAAE 218

RESULT 4

A:Molecule type: DNA

A:Accession: J00622

A:Title: myelin P0 protein precursor - rat

A:Residues: 1-248 <150>

A:Accession: J00622

A:Title: myelin P0 protein precursor - rat

A:Reference number: J00622; MUID:9016682; PMID:1483051

A:Accession: J00622

A:Molecule type: DNA

A:Accession: J00622

A:Title: myelin P0 protein precursor - rat

A:Residues: 1-248 <150>

A:Accession: J00622

A:Title: myelin P0 protein precursor - rat

A:Reference number: J00622; MUID:9016682; PMID:1483051

A:Accession: J00622

A:Molecule type: DNA

A:Accession: J00622

A:Title: myelin P0 protein precursor - rat

A:Residues: 1-248 <150>

A:Accession: J00622

A:Title: myelin P0 protein precursor - rat

A:Reference number: J00622; MUID:9016682; PMID:1483051

A:Accession: J00622

A:Molecule type: DNA

A:Accession: J00622

A:Title: myelin P0 protein precursor - rat

A:Residues: 1-248 <150>

A:Accession: J00622

A:Title: myelin P0 protein precursor - rat

A:Reference number: J00622; MUID:9016682; PMID:1483051

A:Accession: J00622

A:Molecule type: DNA

A:Accession: J00622

A:Title: myelin P0 protein precursor - rat

A:Residues: 1-248 <150>

A:Accession: J00622

A:Title: myelin P0 protein precursor - rat

A:Reference number: J00622; MUID:9016682; PMID:1483051

A:Accession: J00622

A:Molecule type: DNA

A:Accession: J00622

A:Title: myelin P0 protein precursor - rat

A:Residues: 1-248 <150>

A:Accession: J00622

A:Title: myelin P0 protein precursor - rat

A:Reference number: J00622; MUID:9016682; PMID:1483051

A:Accession: J00622

A:Molecule type: DNA

A:Accession: J00622

A:Title: myelin P0 protein precursor - rat

A:Residues: 1-248 <150>

A:Accession: J00622

A:Title: myelin P0 protein precursor - rat

A:Reference number: J00622; MUID:9016682; PMID:1483051

A:Accession: J00622

A:Molecule type: DNA

A:Accession: J00622

A:Title: myelin P0 protein precursor - rat

A:Residues: 1-248 <150>

A:Accession: J00622

A:Title: myelin P0 protein precursor - rat

A:Reference number: J00622; MUID:9016682; PMID:1483051

A:Accession: J00622

A:Molecule type: DNA

A:Accession: J00622

A:Title: myelin P0 protein precursor - rat

A:Residues: 1-248 <150>

A:Accession: J00622

A:Title: myelin P0 protein precursor - rat

InterPro; IPRO07110; Ig-like.
InterPro; IPRO03066; IG MEC.
InterPro; IPRO03986; IG V.
InterPro; IPRO00920; MYELIN_P0.
SMART; SMO0046; MYELIN_P0.
SMART; SMO0406; IGV 1.
PROSITE; PS50835; IG_LIKE_1.
PROSITE; PS50835; IGV_LIKE_1.
Pfam; PF00008; Immunoglobulin domain; Transmembrane; Glycoprotein; SIGNAL

FT CHAIN 1 26 POTENTIAL
FT CHAIN 27 215 POTENTIAL
FT CHAIN 3 215 POTENTIAL
FT TRANSMEM 155 175 POTENTIAL
FT DOMAIN 176 215 CYTOPLASMIC (POTENTIAL)
FT DOMAIN 217 141 IG-LIKE V-YPE
FT DOMAIN 27 141 IG-LIKE V-YPE
FT CATALYTIC 32 139 N-LINKED (GLNAC...) (POTENTIAL)
FT CARDFOOD 33 139 N-LINKED (GLNAC...) (POTENTIAL)
FT CARDFOOD 118 118 N-LINKED (GLNAC...) (POTENTIAL)
FT CARDHYD 215 AA; 24484 MM; 9019EAT98B591SA CRG64;

Query Match 13.1%; Score 147; DB 1; Length 215;
Best Local Similarity 25.7%; Pred. No. 3,7e-06;
Matches 37; Conservative 35; Mismatches 80; Indels 50; Gaps 9;

QY 7 LEPALVILWVSVCPCVCFVSTFVGTPAAGHPALCSCHSREAVTIVTVTFVP 66
21 LAPTA-VETFSV-----LEANGTDARKCTFSRPAVDLNT--WFPEF 67

DB 67 -SGC-DRLIIVGVHCVSHSPFCFLKCGSKGLDVLTNTLVDSGLCYCNUSR 124
68 LDGGPQQPVFIHDPFGSTGRFQVGNRPNDNISLLWLPQDNSTYCQVN 127
QY 125 EEFENAHNFVKTKTLPRSTGRTGRTGRTGRTGRTGRTGRTGRTGRTGRT 170
128 -----FDPGVIGCEIRLSVHVTSFSLIFLAISGACALMIIVI 170

QY 174 LEIMYCVNSVAFESQAQSADYSIALHSNENSVDEVE 215
DB 171 VWVLFFQFKGWASEA-----HVVVELSKKEELNOEK 205

RESULT 12
MYP0_HTRF STANDARD; PRT; 246 AA.

AC F00388, 991 (Rel. 17, Created)
DB 01-FEB-1991 (Rel. 17, Last sequence update)
DT 04-SER-2003 (Rel. 42, Last annotation update)
DE Myelin P0 protein precursor (Myelin protein zero) [Myelin peripheral
OS Homo sapiens] (UniProtKB/Swiss-Prot)
OC Heteroductum francisci (Horn shark)
CC Bakurgeta; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
CC Elasmobranchii; Galeomorphii; Heterodontidae; Heterodontiformes;
CC NCBT TaxID=7782; Heterodontus.
RN NCBI TaxID=7782; [1]
RW SEQUENCE FROM N.A.
RP MEDLINE=9001074; PubMed=247817;
RA Savendra R.J., Fors L., Abersold R.H., Arden B., Horvath S.,
RA Sanders J., Hood L. The myelin proteins of the shark brain are similar to the myelin
PT protein of the mammalian nervous system.;
RL J. Mol. Evol. 29:149-156(1989).
CC -!- FUNCTION: CREATION OF AN EXTRACELLULAR MEMBRANE FACE WHICH GUIDES
CC THE WRAPPING PROCESS AND ULTIMATELY COMPLETES ADJACENT LABELLES.
CC -!- TISSUE SPECIFICITY: FOUND ONLY IN PERIPHERAL NERVOUS SYSTEM
CC SCHWANN CELLS.
CC -!- FMN -N-GLYCAN IS SULFATED (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE MYELIN P0 PROTEIN FAMILY.
CC -!- FUNCTION: BELONGS TO THE MYELIN P0 PROTEIN FAMILY.

CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
 CC between the European Bioinformatics Institute and the Swiss Institute of
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 CC modified and this statement is not removed, usage by and for commercial
 CC entities is prohibited. See <http://www.ebi.ac.uk/ebis/announcements/>
 CC or email to license@ebi.ac.uk.

CC ENBL, X16714; OM37865.1; .
 CC R5SP, P06907; 1HEP.
 CC InterPro: IPR007110; IG-like.
 CC InterPro: IPR003596; IG V.
 CC InterPro: IPR009020; Myelin_P0.
 CC PRINTS: PR00213; MYELINP0.
 CC SMART: SM00406; IG V.
 CC PROSITE: PS00835; IG LIKE, 1.
 CC PROSITE: PS00848; MYELIN P0.
 CC PROSITE: PS00856; MYELIN P0.
 CC KMW phosphorylation; Immunoglobulin domain; Signal.
 CC SIGNAL 1 27 BY SIMILARITY.
 CC DOMAIN 28 246 EXTRACELLULAR (POTENTIAL).
 CC TRANSHEM 151 178 POTENTIAL.
 CC DOMAIN 179 246 CYTOPLASMIC (POTENTIAL).
 CC DOMAIN 247 246 CYTOPLASMIC V-TYPE.
 CC DUF0120 48 123 POTENTIAL.
 CC CARBOHYD 120 120 N-LINKED (GLCNAC. .) (COMPLEX) (BY
 CC SIMILARITY).
 CC SEQUENCE 246 AA; 27335 MW; A76A9EDD430FA CRC64;
 CC
 CC Query Match 12.9%; Score 144.5; DB 1; Length 246;
 CC Best Local Similarity 25.8%; Pred. No. 7.2e-06;
 CC Matches 49; Conservative 37; Mismatches 77; Indels 27; Gaps 7;
 CC
 CC QY 16 IYWSVCPVEVSETEAVQ-----GNFMKLSCKSEKVEAVTVEMFRP 66
 CC DB 10 LFCECLVAFVSALFQSSISVTHNLUHTVGSVDLYLC-GPMSNEVSDUTLSMRFP 68
 CC
 CC QY 67 EGKDEL-IYEVKSHQVE--SPQGLQWNSKLOQVSTLVNLSGLATCVNS 123
 CC DB 68 DNRHIIISIFHFGQVIEKQVQGVGVGVSDIISDQSSIVIRVLDYNTGTFCDVX 128
 CC
 CC QY 124 RFETAEHAFVKTALPLVAVTES-----AGEPTSVSEHMLVAVLTMLLEKI 178
 CC DB 129 NFPD-----VGTSSDHLVTVDPKPGVGVSGAIGTQGHILLVVGXLY--FR 179
 CC
 CC QY 179 VYKRVNSAE 188
 CC DB 180 VYVREHSE 189

CC RESULT 13
 CC MYD, CHICK, CHICK STANDARD; PRT; 249 AA.
 CC AD P37361;
 CC DT 01-OCT-1994 (Rel. 30, Created)
 CC DT 01-OCT-1994 (Rel. 30, Last sequence update)
 CC DT 01-OCT-1994 (Rel. 30, Last annotation update)
 CC DE Myelin P0 protein precursor (Myelin protein zero) (Myelin peripheral
 CC protein) (MPP).
 CC OS Gallus gallus (Chicken).
 CC OC Chordata; Craniata; Vertebrata; Rutelesotomi;
 CC OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Gallus;
 CC OC Gallus.
 CC CO NCBI_TaxID=9031;
 CC RN
 CC RP SEQUENCE FROM N.A.
 CC RX MEDLINE=90204597; PubMed=1690817;
 CC RA Baber M.F.X., Schauer T., Gattrell W.A.,
 CC RT Nucleotide cloning of cDNAs that encode the chicken P0 protein:
 CC ET evidence for early expression in avians.;

CC J. Neurosci. Res. 25:143-151(1990).
 CC -1- FUNCTION: CREATION OF AN EXTRACELLULAR MEMBRANE RACE WHICH GUIDES
 CC MYELINATION OF AXONS AND DENDrites. COMPLEXES AND/OR LAMINAE.
 CC -1- SUBCELLULAR LOCATION: Type 1 membrane protein.
 CC -1- TISSUE SPECIFICITY: FOUND ONLY IN PERIPHERAL NERVOUS SYSTEM
 CC -1- SCHWANN CELLS.
 CC -1- SIMILARITY: Belongs to immunoglobulin-like V-type domain.
 CC -1- SIMILARITY: BELONGS TO THE MYELIN P0 PROTEIN FAMILY.
 CC PIR: A61087; A61087.
 CC R5SP, P06907; 1HEP.
 CC InterPro: IPR007110; IG-like.
 CC InterPro: IPR003596; IG V.
 CC InterPro: IPR009020; Myelin_P0.
 CC PRINTS: PR00213; MYELINP0.
 CC SMART: SM00406; IG V.
 CC PROSITE: PS00835; IG LIKE, 1.
 CC PROSITE: PS00848; MYELIN P0.
 CC PROSITE: PS00856; MYELIN P0.
 CC KMW phosphorylation; Immunoglobulin domain; Signal.
 CC SIGNAL 1 27 BY SIMILARITY.
 CC DOMAIN 28 246 EXTRACELLULAR (POTENTIAL).
 CC TRANSHEM 151 178 POTENTIAL.
 CC DOMAIN 179 246 CYTOPLASMIC.
 CC DOMAIN 247 246 CYTOPLASMIC V-TYPE.
 CC DUF0120 48 123 POTENTIAL.
 CC CARBOHYD 122 122 N-LINKED (GLCNAC. .) (POTENTIAL).
 CC SEQUENCE 249 AA; 27466 MW; FED1401FPA08FB CRC64;
 CC
 CC Query Match 12.5%; Score 140.5; DB 1; Length 249;
 CC Best Local Similarity 23.6%; Pred. No. 1.7e-05;
 CC Matches 48; Conservative 43; Mismatches 87; Indels 23; Gaps 8;
 CC
 CC QY 13 IYLVIVSVCP-----NCTVSESTEAQVGNHMLCSCSKSEKVEAVTVEMFRP 67
 CC DB 13 LLVGLLSASQSPTLAHVTPVYGVTVGSHTVLC-SFNSSEMSIEDISYTHFQAE 71
 CC
 CC QY 68 GQVDEL-IYEVKSHQVE--SPQGLQWNSKLOQVSTLVNLSGLATCVNS 124
 CC DB 72 SREISISIFHFGQVSDIISDQSSIVIRVLDYNTGTFCDVX 131
 CC
 CC QY 125 RFETAEHAFVKTALPLVAVTES-----AGEPTSVSEHMLVAVLTMLLEKI 181
 CC DB 132 PPD-----VGTSSDHLVTVDPKPGVGVSGAIGTQGHILLVVGXLY--FR 185
 CC
 CC QY 182 -----RQVREHSE 197
 CC DB 186 RQVLRRLSASQKLRQARD 208

CC RESULT 14
 CC CIB2, RAT STANDARD; PRT; 215 AA.
 CC ID CIB2, RAT
 CC DT 01-OCT-1996 (Rel. 34, Created)
 CC DT 01-OCT-1996 (Rel. 34, Last sequence update)
 CC DT 15-SEP-2003 (Rel. 42, Last annotation update)
 CC DE Sodium channel beta-2 subunit precursor.
 CC OS Rattus norvegicus (rat).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Rutelesotomi;
 CC OC Mammalia; Sauria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CC CO NCBI_TaxID=10101;
 CC RN
 CC RP SEQUENCE FROM N.A., AND SEQUENCE OF 30-58; 95-134 AND 142-151.
 CC RX MEDLINE=94067641; PubMed=8521473; Westendbrook R.E.,
 CC RA Baber M.F.X., Schauer T., Gattrell W.A.,
 CC RT "Structure and function of the beta 2 subunit of brain sodium
 CC channels, a transmembrane glycoprotein with a CM motif.";
 CC Cell 83:443-442(1995).

EX MEDLINE:22354683; PubMed:12466851;
 SA The RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 KT 60,770 full-length cDNAs";
 DR ENBL; AK049742; BAC13901.1; -;
 DR ENBL; AK076466; BAC13901.1; -;
 SQ SEQUENCE 215 AA; 24789 MW; 08D7B4704178A43 CRC64;

Query Match 97.68; Score 1097; DB 11; Length 215;
 Best Local Similarity 97.18; Pred. No. 6.7e-107;
 Matches 210; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 MPANRPLFLASLVLIWVSCFVPCVSETEAVQGNPKLSCISOMREVEATTV 60
 DB 1 MPANRPLFLASLVLIWVSCFVPCVSETEAVQGNPKLSCISOMREVEATTV 60
 QY 61 EWFYRPSGKQDFIYVNRGHGVSEPPQRLQNGSKDLQVSIYVNTLINDSGLYTC 120
 DB 61 EWFYRPSGKQDFIYVNRGHGVSEPPQRLQNGSKDLQVSIYVNTLINDSGLYTC 120
 QY 61 EWFYRPSGKQDFIYVNRGHGVSEPPQRLQNGSKDLQVSIYVNTLINDSGLYTC 120
 DB 61 EWFYRPSGKQDFIYVNRGHGVSEPPQRLQNGSKDLQVSIYVNTLINDSGLYTC 120
 QY 122 NVSSEFEFNRFPVKTLLIPLVTEAGEDFTVSVSEIMYLLVLTWLLMETIC 180
 DB 122 NVSSEFEFNRFPVKTLLIPLVTEAGEDFTVSVSEIMYLLVLTWLLMETIC 180
 QY 121 NVKREVEEENQASNDYLLIPLVTEAGEDFTVSVSEIMYLLVLTWLLMETIC 180
 DB 121 NVKREVEEENQASNDYLLIPLVTEAGEDFTVSVSEIMYLLVLTWLLMETIC 180
 QY 181 YRKYSKAEENQASNDYLAIPSENKNSAVPVEE 215
 DB 181 YRKYSKAEENQASNDYLAIPSENKNSAVPVEE 215

RESULT 5
 ID Q91299 PRELIMINARY; PRT; 215 AA.
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 OS Brain and olfactory system, channel, beta 3 subunit.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Sciuromorphi; Muridae; Mus.
 NCBI_TaxID=10090;
 RP SEQUENCE FROM N.A.
 RA Chen C., Avery C., Kazen-Gillespie K., Idom L.L.;
 RT Mouse brain and olfactory system, channel, beta 3 subunit.
 DR ENBL; AY049036; AAL07512.1; -;
 DR InterPro; IPR003599; I9-like
 DR InterPro; IPR003599; I9-like
 DR Pfam; PF00047; I9; 1; Ig_MHC.
 DR SMART; SM00409; IG; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 SQ SEQUENCE 215 AA; 24771 MW; 089BEA704178A432 CRC64;

Query Match 97.18; Score 1097; DB 11; Length 215;
 Best Local Similarity 97.18; Pred. No. 6.7e-107;
 Matches 209; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 1 MPANRPLFLASLVLIWVSCFVPCVSETEAVQGNPKLSCISOMREVEATTV 60
 DB 1 MPANRPLFLASLVLIWVSCFVPCVSETEAVQGNPKLSCISOMREVEATTV 60
 QY 61 EWFYRPSGKQDFIYVNRGHGVSEPPQRLQNGSKDLQVSIYVNTLINDSGLYTC 120
 DB 61 EWFYRPSGKQDFIYVNRGHGVSEPPQRLQNGSKDLQVSIYVNTLINDSGLYTC 120
 QY 122 NVSSEFEFNRFPVKTLLIPLVTEAGEDFTVSVSEIMYLLVLTWLLMETIC 180
 DB 122 NVSSEFEFNRFPVKTLLIPLVTEAGEDFTVSVSEIMYLLVLTWLLMETIC 180

Query Match 97.18; Score 1097; DB 11; Length 215;
 Best Local Similarity 97.18; Pred. No. 6.7e-107;
 Matches 209; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 1 MPANRPLFLASLVLIWVSCFVPCVSETEAVQGNPKLSCISOMREVEATTV 60
 DB 1 MPANRPLFLASLVLIWVSCFVPCVSETEAVQGNPKLSCISOMREVEATTV 60
 QY 61 EWFYRPSGKQDFIYVNRGHGVSEPPQRLQNGSKDLQVSIYVNTLINDSGLYTC 120
 DB 61 EWFYRPSGKQDFIYVNRGHGVSEPPQRLQNGSKDLQVSIYVNTLINDSGLYTC 120
 QY 122 NVSSEFEFNRFPVKTLLIPLVTEAGEDFTVSVSEIMYLLVLTWLLMETIC 180
 DB 122 NVSSEFEFNRFPVKTLLIPLVTEAGEDFTVSVSEIMYLLVLTWLLMETIC 180

QY 181 YRKYSKAEENQASNDYLAIPSENKNSAVPVEE 215
 DB 181 YRKYSKAEENQASNDYLAIPSENKNSAVPVEE 215

RESULT 6
 ID Q9M42 PRELIMINARY; PRT; 185 AA.
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Sciuromorphi; Muridae; Homo.
 NCBI_TaxID=9606;
 RP SEQUENCE FROM N.A.
 RA TSSUP-Kidney;
 DR ENBL; BC021266; AA021266.1; -;
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; I9; 1; Ig_MHC.
 DR SMART; SM00409; IG; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 SQ SEQUENCE 185 AA; 21497 MW; CFE98510DC59800 CRC64;

Query Match 97.48; Score 420; DB 4; Length 185;
 Best Local Similarity 49.58; Pred. No. 6.4e-36;
 Matches 90; Conservative 30; Mismatches 54; Indels 8; Gaps 5;
 QY 42 KLRCSOMREVEATTVWFPRGKQDFIYVNRGHGVSEPPQRLQNGSKDLQVSIYVNTLINDSGLYTC 120
 DB 4 KLRCSOMREVEATTVWFPRGKQDFIYVNRGHGVSEPPQRLQNGSKDLQVSIYVNTLINDSGLYTC 120
 QY 98 --KDLQVSIYVNTLINDSGLYTCVNRSEFEFNRFPVKTLLIPLVTEAGEDFTVSVSEIMYLLVLTWLLMETIC 155
 DB 98 --KDLQVSIYVNTLINDSGLYTCVNRSEFEFNRFPVKTLLIPLVTEAGEDFTVSVSEIMYLLVLTWLLMETIC 155
 QY 64 GTKDLQVSIYVNTLINDSGLYTCVNRSEFEFNRFPVKTLLIPLVTEAGEDFTVSVSEIMYLLVLTWLLMETIC 123
 DB 64 GTKDLQVSIYVNTLINDSGLYTCVNRSEFEFNRFPVKTLLIPLVTEAGEDFTVSVSEIMYLLVLTWLLMETIC 123
 QY 156 VNSIMYLLVLTWLLMETICVNRSEFEFNRFPVKTLLIPLVTEAGEDFTVSVSEIMYLLVLTWLLMETIC 180
 DB 156 VNSIMYLLVLTWLLMETICVNRSEFEFNRFPVKTLLIPLVTEAGEDFTVSVSEIMYLLVLTWLLMETIC 180
 QY 124 TSSUP-KIDNEY; Muridae; Mus.
 DB 124 TSSUP-KIDNEY; Muridae; Mus.

Query Match 97.48; Score 420; DB 4; Length 185;
 Best Local Similarity 49.58; Pred. No. 6.4e-36;
 Matches 90; Conservative 30; Mismatches 54; Indels 8; Gaps 5;
 QY 42 KLRCSOMREVEATTVWFPRGKQDFIYVNRGHGVSEPPQRLQNGSKDLQVSIYVNTLINDSGLYTC 120
 DB 4 KLRCSOMREVEATTVWFPRGKQDFIYVNRGHGVSEPPQRLQNGSKDLQVSIYVNTLINDSGLYTC 120
 QY 98 --KDLQVSIYVNTLINDSGLYTCVNRSEFEFNRFPVKTLLIPLVTEAGEDFTVSVSEIMYLLVLTWLLMETIC 155
 DB 98 --KDLQVSIYVNTLINDSGLYTCVNRSEFEFNRFPVKTLLIPLVTEAGEDFTVSVSEIMYLLVLTWLLMETIC 155
 QY 64 GTKDLQVSIYVNTLINDSGLYTCVNRSEFEFNRFPVKTLLIPLVTEAGEDFTVSVSEIMYLLVLTWLLMETIC 123
 DB 64 GTKDLQVSIYVNTLINDSGLYTCVNRSEFEFNRFPVKTLLIPLVTEAGEDFTVSVSEIMYLLVLTWLLMETIC 123
 QY 156 VNSIMYLLVLTWLLMETICVNRSEFEFNRFPVKTLLIPLVTEAGEDFTVSVSEIMYLLVLTWLLMETIC 180
 DB 156 VNSIMYLLVLTWLLMETICVNRSEFEFNRFPVKTLLIPLVTEAGEDFTVSVSEIMYLLVLTWLLMETIC 180
 QY 124 TSSUP-KIDNEY; Muridae; Mus.
 DB 124 TSSUP-KIDNEY; Muridae; Mus.

Query Match 97.48; Score 420; DB 4; Length 185;
 Best Local Similarity 49.58; Pred. No. 6.4e-36;
 Matches 90; Conservative 30; Mismatches 54; Indels 8; Gaps 5;
 QY 42 KLRCSOMREVEATTVWFPRGKQDFIYVNRGHGVSEPPQRLQNGSKDLQVSIYVNTLINDSGLYTC 120
 DB 4 KLRCSOMREVEATTVWFPRGKQDFIYVNRGHGVSEPPQRLQNGSKDLQVSIYVNTLINDSGLYTC 120
 QY 98 --KDLQVSIYVNTLINDSGLYTCVNRSEFEFNRFPVKTLLIPLVTEAGEDFTVSVSEIMYLLVLTWLLMETIC 155
 DB 98 --KDLQVSIYVNTLINDSGLYTCVNRSEFEFNRFPVKTLLIPLVTEAGEDFTVSVSEIMYLLVLTWLLMETIC 155
 QY 64 GTKDLQVSIYVNTLINDSGLYTCVNRSEFEFNRFPVKTLLIPLVTEAGEDFTVSVSEIMYLLVLTWLLMETIC 123
 DB 64 GTKDLQVSIYVNTLINDSGLYTCVNRSEFEFNRFPVKTLLIPLVTEAGEDFTVSVSEIMYLLVLTWLLMETIC 123
 QY 156 VNSIMYLLVLTWLLMETICVNRSEFEFNRFPVKTLLIPLVTEAGEDFTVSVSEIMYLLVLTWLLMETIC 180
 DB 156 VNSIMYLLVLTWLLMETICVNRSEFEFNRFPVKTLLIPLVTEAGEDFTVSVSEIMYLLVLTWLLMETIC 180
 QY 124 TSSUP-KIDNEY; Muridae; Mus.
 DB 124 TSSUP-KIDNEY; Muridae; Mus.


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RA Strauberg R.;
RL Submitted (APR-2001) to the RMBL/GenBank/DBJ databases.
DR Accession: AF049311.1
DR HSP: P06907; INEU
DB 11 ASLVLTAVTDEIVGAVGSKVTLHC-SFWSSEWDDISFTWYQEGR 70
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig-MHC.
DR InterPro: IPR003036; Ig-V.
DR InterPro: IPR000920; Myelin_P0.
DR Pfam: PF00047; Ig_1.
DR SMART: PR00213; MYELINP0.
DR PRINTS: SM00406; IG; 1 LK.
DR SMART: SM00406; IG; 1 LK.
DR PROSITE: PS00565; MYELIN_P0; 1.
DR PROSITE: PS00565; MYELIN_P0; 1.
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Query Match
Best Local Similarity 28.3%; Pos: 33; Mismatches 81; Indels 23; Gaps 258;
Matches 54; Conservative 33;
QY 11 ASLVLTAVTDEIVGAVGSKVTLHC-SFWSSEWDDISFTWYQEGR 70
DB 30 SSVLV-----SPAQLVTVTDEIVGAVGSKVTLHC-SFWSSEWDDISFTWYQEGR 84
QY 71 DFL-IYFYMHOEVE-SFQGLQNSKDLQNSVTLVTLNDSGLYTCNSRFE 127
DB 85 DAISIFVAGQPVDEIVGTFKELQVQCPKWKOSIVTINLDSYNSFTCVKNPFD 144
QY 128 FEHPPFVATRTLLITREAGDFTSVSEIMMYTLVFLVFLMLIEM-YCY----- 181
DB 145 -----IVKTSQVTLVPRFPYRFGVAGVGLGVLVLLLVFLVYVTCURQA 198
QY 182 ----RKVSKEE 189
DB 199 MLCNRDAMEN 209
QY 182 ----RKVSKEE 189
DB 199 MLCNRDAMEN 209
RESULT 11
QY 026777 PRELIMINARY; PRT; 225 AA.
ID Q32677;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE Major peripheral myelin protein (PO) (Scargem).
DE Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
NCBI_Taxid:6031;
RN [1]
RS SCQUENCE FROM N.A.
RA Strittmann A., Jeserich G.
EA "Molecular cloning and tissue expression of a cDNA encoding IPI--a P0-
ET like glycoprotein of trout CNS myelin";
ET J. Neurochem. 63:1938-1956 (1995).
DR EMBL: S78261; SABS4359.1; .
DR HSP: P06907; INEU.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig-MHC.
DR InterPro: IPR003596; Ig-V.
DR InterPro: IPR000920; Myelin_P0.
DR Pfam: PF00047; Ig_1.
DR SMART: PR00213; MYELINP0.
DR SMART: SM00406; IG; 1 LK.
DR PROSITE: PS00565; IG_LIKE; 1.
SQ
Query Match
Best Local Similarity 13.3%; Score 160; DB 13; Length 202;
Matches 46; Conservative 49; Mismatches 81; Indels 32; Gaps 7;
QY 7 LPLAGLQVLTWVSCVFCVVEVSETEV-----QQLMKLISCKHREVE 55
DB 4 ILALAVLL-----GLVQSEAVITVMEHRLGDLISGFSWNTSD 53
QY 56 ATTVTFPTEGKDFL-IYFYMHOEVE-SFQGLQNSKDLQNSVTLVTL 112
DB 54 DTVT-PSWVSGEEDALSIETGCPYDNKGFPEELFVPSGRGSLILAD 110
QY 113 NUSGLTVTSREFFENRFPK--TTLTLPVLTVEAGDFTSVSEIMMYTLV 170
DB 113 GNGTFPCNKNPFDVGRASSVLTVPFVQVGTGSLGGLLVLLVILV 172
QY 171 LMLIEMT-----CYRKVSKEEAAQE 193
DB 173 RPLVARYPLSVSGKNGKGGKGGSQ 200
QY 171 LMLIEMT-----CYRKVSKEEAAQE 193
DB 173 RPLVARYPLSVSGKNGKGGKGGSQ 200
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QY 031406 PRELIMINARY; PRT; 202 AA.
ID Q31406;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE LMA-2003 (TrEMBLrel. 23, Last annotation update)
DR IPI
GN IPI.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
NCBI_Taxid:6031;
RN [1]
RS SCQUENCE FROM N.A.
RA Strittmann A., Jeserich G.
EA "Molecular cloning and tissue expression of a cDNA encoding IPI--a P0-
ET like glycoprotein of trout CNS myelin";
ET J. Neurochem. 63:1938-1956 (1995).
DR EMBL: S78261; SABS4359.1; .
DR HSP: P06907; INEU.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig-MHC.
DR InterPro: IPR003596; Ig-V.
DR InterPro: IPR000920; Myelin_P0.
DR Pfam: PF00047; Ig_1.
DR SMART: PR00213; MYELINP0.
DR SMART: SM00406; IG; 1 LK.
DR PROSITE: PS00565; IG_LIKE; 1.
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Query Match
Best Local Similarity 22.1%; Pred No. 1.6e-07;
Matches 46; Conservative 49; Mismatches 81; Indels 32; Gaps 7;
QY 7 LPLAGLQVLTWVSCVFCVVEVSETEV-----QQLMKLISCKHREVE 55
DB 4 ILALAVLL-----GLVQSEAVITVMEHRLGDLISGFSWNTSD 53
QY 56 ATTVTFPTEGKDFL-IYFYMHOEVE-SFQGLQNSKDLQNSVTLVTL 112
DB 54 DTVT-PSWVSGEEDALSIETGCPYDNKGFPEELFVPSGRGSLILAD 110
QY 113 NUSGLTVTSREFFENRFPK--TTLTLPVLTVEAGDFTSVSEIMMYTLV 170
DB 113 GNGTFPCNKNPFDVGRASSVLTVPFVQVGTGSLGGLLVLLVILV 172
QY 171 LMLIEMT-----CYRKVSKEEAAQE 193
DB 173 RPLVARYPLSVSGKNGKGGKGGSQ 200
QY 171 LMLIEMT-----CYRKVSKEEAAQE 193
DB 173 RPLVARYPLSVSGKNGKGGKGGSQ 200
RESULT 13
QY 031406 PRELIMINARY; PRT; 215 AA.
ID Q31406;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Created)

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DT	01-DRC-2001 (TREMURel. 19, Last sequence update)
DT	01-WAR-2003 (TREMURel. 23, Last annotation update)
DT	Epithelial V-like antigen.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NC	AB1_TaxID=10090;
NC	AB1_TaxID=10090;
RP	SEQUENCE FROM N.A.
RP	TISSUE=Salivary gland;
RA	Strausberg R.
RA	Submitted (Oct-2001) to the EMBL/GenBank/DBS databases.
RP	SEQUENCE FROM N.A.
RP	STRAIN=C57BL/6J; TISSUE=mesonephros;
RP	STRAIN=C57BL/6J; TISSUE=mesonephros;
RA	The PANTOM Consortium.
RA	The RIKEN Genome Exploration Research Group Phase I & II Team;
FT	Analysis of the mouse transcriptome based on functional annotation of
FT	the mouse transcriptome based on functional annotation of
RL	Nature 420:563-573 (2003).
RL	EMBL; BC015076; AAH15076.1; --
DR	EMBL; AK032788; BAC28022.1; --
DR	InterPro; IPR007119; Ig-like.
DR	InterPro; IPR003008; Ig_MHC.
DR	InterPro; IPR003596; Ig_V.
DR	InterPro; IPR003596; Ig_V.
DR	Pfam; PF00047; Ig; Myelin_P0.
DR	PRINTS; PR00213; MYELINP0.
DR	SMART; SM00406; IGV; 1..186
DR	SMART; PS3195; IGV; 1..186
SQ	SEQUENCE -215 AA, 23182; P05E56787C79C4 CIRC44;
Query Match	13.13% Score 147; DR 11; Length 215;
Best Local Similarity	22.4%; Pred. No. 3.5e-07;
Matches	47; Conservative 45; Mismatches 101; Indels 8; Gaps 5;
QY	10 LAGSLVITVGSFCVFCV--PSTETANGKPKLCISCHREAVTIVEMFRP- 66
DY	10 LPILLSSGLCTFATVETVITSGLVNGLVSGVSSAPGVATV--VFRR 68
DY	10 LAGSLVITVGSFCVFCV--PSTETANGKPKLCISCHREAVTIVEMFRP- 66
DY	67 EGGKD-FLVTEYGVNEVSFPQRLWNGSKGLQVSIIVLVNLSGVTYCNWSR 125
DY	69 DQMGQVTFTHMDFPQSGQRKRVWQGPRTDVLMLLFQDFMGTTCVQMP 128
QY	126 FTEAHRRFVKTLLFLPLAVTTEAGDFSTVSEIMVLLVLLLELITCYKVS 185
DY	129 FTEAHRRFVKTLLFLPLAVTTEAGDFSTVSEIMVLLVLLLELITCYKVS 185
QY	186 KAEVAAQGNASVLAIPSENK 206
DY	186 SHAGAGTGSKEZKQNGK 206
RESULT 14	QYAVN3 PRELIMINARY; PRT; 229 AA.
AC	QYAVN3 PRELIMINARY; PRT; 229 AA.
DT	01-WAR-2003 (TREMURel. 23, Created)
DT	01-WAR-2003 (TREMURel. 23, Last sequence update)
DT	01-WAR-2003 (TREMURel. 25, Last annotation update)
DE	Hypothetical protein.
DE	Xenopus laevis (African clawed frog).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Amphibia; Anura; Mesobatrachia; Pipiloide; Pipidae;
OC	Xenopodinae; Xenopus.
NC	NCBI_TaxID=8155;
NC	NCBI_TaxID=8155;
RP	SEQUENCE FROM N.A.
RP	TISSUE=embryo;
RA	Klein S., Strausberg R.;

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Db      173 DYTGCSTSESLSPVKQAPRKSPDTEGLVKSLPSGSHQIPVI 214
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Search completed: December 5, 2003, 23:22:33

Search completed: Done
Job time : 112 secs

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3 PRIOR FILING DATE: 1998-05-07
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8 PRIOR FILING DATE: 1998-06-02
9 PRIOR APPLICATION NUMBER: 60/087759
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11 PRIOR FILING DATE: 1998-06-02
12 PRIOR FILING DATE: 1998-06-02
13 PRIOR APPLICATION NUMBER: 60/087827
14 PRIOR FILING DATE: 1998-06-04
15 PRIOR APPLICATION NUMBER: 60/088021
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60 PRIOR FILING DATE: 1998-06-12
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88 PRIOR FILING DATE: 1998-06-19
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92 PRIOR FILING DATE: 1998-06-22
93 PRIOR APPLICATION NUMBER: 60/090252
94 PRIOR FILING DATE: 1998-06-22
95 PRIOR APPLICATION NUMBER: 60/090254
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97 PRIOR APPLICATION NUMBER: 60/090349
98 PRIOR FILING DATE: 1998-06-23
99 PRIOR APPLICATION NUMBER: 60/090355
100 PRIOR FILING DATE: 1998-06-23
101 PRIOR APPLICATION NUMBER: 60/090429
102 PRIOR FILING DATE: 1998-06-24
103 PRIOR APPLICATION NUMBER: 60/090431
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131 PRIOR APPLICATION NUMBER: 60/090696
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144 PRIOR FILING DATE: 1998-07-02
145 PRIOR APPLICATION NUMBER: 60/091626
146 PRIOR FILING DATE: 1998-07-02
147 PRIOR APPLICATION NUMBER: 60/091633
148 PRIOR FILING DATE: 1998-07-02


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RESULT 5
US-09-430-503-8
; Sequence 44, Application US/09410503
; Patent No. 6355786
; GENERAL INFORMATION:
; APPLICANT: Zhao, Zhizhuang
; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND
; TITLE OF INVENTION: THERAPEUTIC AND SCREENING METHODS USING SAME
; FILE REFERENCE: Attorney Docket No. 6355786 1242-11/2
; CURRENT FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 269
; BEST LOCAL SIMILARITY 26.0%; Pred. No. 4,4e-06;
; ORGANISM: Homo sapiens
US-09-430-503-8
Query Match 11.5%; Score 131; DB 4; Length 269;
Best Local Similarity 23.0%; Pred. No. 4,1e-06;
Matches 51; Conservative 32; Mismatches 81; Indels 58; Gaps 9;
QY 27 VVPSSTEAHQVQHPKMLACISCKMREVEAT---TVVEMFRPFGGKQPL-IYEVNQH 82
DB 40 VYTKPEIFVANGTQKLTIC---KFKSTSTGGLTSGMSFGQEGADTVSFFHSQGV 95
DB 96 YLQNFPPKDHISNAGLKKDASINENMQFHNGTYCDVNN----- 139
QY 141 IPLAVTEAGEDFTFSVSE-----IMMILLVFTLMLLIEMICY---RNVSKA 187
DB 140 -PDDIVQVGHIELVYVEKENLPVFPVWVGIVTAVVLGLTLLSNILAVYRNRSKA 198
QY 27 VVPSSTEAHQVQHPKMLACISCKMREVEAT---TVVEMFRPFGGKQPL-IYEVNQH 82
DB 40 VYTKPEIFVANGTQKLTIC---KFKSTSTGGLTSGMSFGQEGADTVSFFHSQGV 95
DB 96 YLQNFPPKDHISNAGLKKDASINENMQFHNGTYCDVNN----- 139
QY 141 IPLAVTEAGEDFTFSVSE-----IMMILLVFTLMLLIEMICY---RNVSKA 187
DB 140 -PDDIVQVGHIELVYVEKENLPVFPVWVGIVTAVVLGLTLLSNILAVYRNRSKA 198
QY 184 -----VSKASEAAGNASD-----YLATPSKENSASV 211
DB 199 DYTQCTGTSBSLSFPVQKRSKPSDTEGLVSPGSGHQGPVI 240

RESULT 6
US-09-430-503-44
; Sequence 44, Application US/09410503
; Patent No. 6355786
; GENERAL INFORMATION:
; APPLICANT: Zhao, Zhizhuang
; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND
; TITLE OF INVENTION: THERAPEUTIC AND SCREENING METHODS USING SAME
; FILE REFERENCE: Attorney Docket No. 6355786 1242-11/2
; CURRENT FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 199
; BEST LOCAL SIMILARITY 26.0%; Pred. No. 4,4e-06;
; ORGANISM: Homo sapiens
US-09-430-503-44
Query Match 11.5%; Score 129; DB 4; Length 199;
Best Local Similarity 26.0%; Pred. No. 4,4e-06;
Matches 47; Conservative 21; Mismatches 73; Indels 40; Gaps 7;
QY 27 VVPSSTEAHQVQHPKMLACISCKMREVEAT---TVVEMFRPFGGKQPL-IYEVNQH 82
DB 40 VYTKPEIFVANGTQKLTIC---KFKSTSTGGLTSGMSFGQEGADTVSFFHSQGV 95
DB 96 YLQNFPPKDHISNAGLKKDASINENMQFHNGTYCDVNN----- 139
QY 141 IPLAVTEAGEDFTFSVSE-----IMMILLVFTLMLLIEMICY---RNVSKA 187
DB 140 -PDDIVQVGHIELVYVEKENLPVFPVWVGIVTAVVLGLTLLSNILAVYRNRSKA 198
QY 188 B 188
DB 199 D 199

RESULT 8
US-09-430-503-42
; Sequence 42, Application US/09430503
; Patent No. 6355786
; GENERAL INFORMATION:
; APPLICANT: Zhao, Zhizhuang
; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND
; TITLE OF INVENTION: THERAPEUTIC AND SCREENING METHODS USING SAME
; FILE REFERENCE: Attorney Docket No. 6355786 1242-11/2
; CURRENT FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 199
; BEST LOCAL SIMILARITY 26.0%; Pred. No. 7,3e-06;
; ORGANISM: Homo sapiens
US-09-430-503-42
Query Match 11.3%; Score 127; DB 4; Length 199;
Best Local Similarity 26.0%; Pred. No. 7,3e-06;
Matches 47; Conservative 21; Mismatches 73; Indels 40; Gaps 7;
QY 27 VVPSSTEAHQVQHPKMLACISCKMREVEAT---TVVEMFRPFGGKQPL-IYEVNQH 82
DB 40 VYTKPEIFVANGTQKLTIC---KFKSTSTGGLTSGMSFGQEGADTVSFFHSQGV 95
DB 96 YLQNFPPKDHISNAGLKKDASINENMQFHNGTYCDVNN----- 139
QY 141 IPLAVTEAGEDFTFSVSE-----IMMILLVFTLMLLIEMICY---RNVSKA 187
DB 140 -PDDIVQVGHIELVYVEKENLPVFPVWVGIVTAVVLGLTLLSNILAVYRNRSKA 198

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Db 40 VYTFKEIFVANGQKGLTCKT---KFKSTSTTGLTSVMSFQPGADATTVSFPHSQGV 95
QY 83 EVES--PFQGLQKNSKDLQVSTVLNVLTNSGLYTCNVSREFEFAHRPPVKTEL 140
Db 96 YLGNVFPFQRIASHAGLDKQASININMNOFTNGTYICDVN----- 139
QY 141 IPLRVTEAGEDFTSVSE-----IMWILLVFLMLLIEMICY--RKVSKA 187
Db 140 -PDDVVGQGHIRYVVEKENLPFVFWVWVGIVTAVVLGLTLLISMLAVLYRNSKR 198
QY 188 E 188
Db 199 D 199

RESULT 9
US-09-430-503-46
; Sequence 46, Application US/09430503
; Patent No. 6355786
; APPLICANT: ZHAO, Zhizhuang
; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND
; TITLE OF INVENTION: THERAPEUTIC AND SCREENING METHODS USING SAME
; FILE REFERENCE: Actonway Docket No. 6355786 1242-11/2
; CURRENT APPLICATION NUMBER: US/09/430,503
; CURRENT FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 49
; SEQ ID NO 46
; ORGANISM: Homo sapiens
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-430-503-46

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Query Match
Best Local Similarity 11.3%; Score 127; DB 4; Length 199;
Matches 47; Conservative 21; Mismatches 73; Indels 40; Gaps 7;
QY 27 VEVFSETEAVGNPKMLKICSMKREVEAT--TVVWFYFPGKGDFL-IYEVNGHQ 82
Db 40 VYTFKEIFVANGQKGLTCKT---KFKSTSTTGLTSVMSFQPGADATTVSFPHSQGV 95
QY 83 EVES--PFQGLQKNSKDLQVSTVLNVLTNSGLYTCNVSREFEFAHRPPVKTEL 140
Db 96 YLGNVFPFQRIASHAGLDKQASININMNOFTNGTYICDVN----- 139
QY 141 IPLRVTEAGEDFTSVSE-----IMWILLVFLMLLIEMICY--RKVSKA 187
Db 140 -PDDVVGQGHIRYVVEKENLPFVFWVWVGIVTAVVLGLTLLISMLAVLYRNSKR 198
QY 188 E 188
Db 199 D 199

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RESULT 10
US-09-430-503-18
; Sequence 18, Application US/09430503
; Patent No. 6355786
; APPLICANT: ZHAO, Zhizhuang
; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND
; TITLE OF INVENTION: THERAPEUTIC AND SCREENING METHODS USING SAME
; FILE REFERENCE: Actonway Docket No. 6355786 1242-11/2
; CURRENT APPLICATION NUMBER: US/09/430,503
; CURRENT FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 49
; SEQ ID NO 18
; ORGANISM: Homo sapiens
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens

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US-09-430-503-18
Query Match
Best Local Similarity 11.3%; Score 127; DB 4; Length 209;
Matches 47; Conservative 21; Mismatches 73; Indels 40; Gaps 7;
QY 27 VEVFSETEAVGNPKMLKICSMKREVEAT--TVVWFYFPGKGDFL-IYEVNGHQ 82
Db 40 VYTFKEIFVANGQKGLTCKT---KFKSTSTTGLTSVMSFQPGADATTVSFPHSQGV 95
QY 83 EVES--PFQGLQKNSKDLQVSTVLNVLTNSGLYTCNVSREFEFAHRPPVKTEL 140
Db 96 YLGNVFPFQRIASHAGLDKQASININMNOFTNGTYICDVN----- 139
QY 141 IPLRVTEAGEDFTSVSE-----IMWILLVFLMLLIEMICY--RKVSKA 187
Db 140 -PDDVVGQGHIRYVVEKENLPFVFWVWVGIVTAVVLGLTLLISMLAVLYRNSKR 198
QY 188 E 188
Db 199 D 199

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RESULT 11
US-09-430-503-20
; Sequence 20, Application US/09430503
; Patent No. 6355786
; APPLICANT: ZHAO, Zhizhuang
; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND
; TITLE OF INVENTION: THERAPEUTIC AND SCREENING METHODS USING SAME
; FILE REFERENCE: Actonway Docket No. 6355786 1242-11/2
; CURRENT APPLICATION NUMBER: US/09/430,503
; CURRENT FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 49
; SEQ ID NO 20
; ORGANISM: Homo sapiens
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-430-503-20

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Query Match
Best Local Similarity 11.3%; Score 127; DB 4; Length 209;
Matches 47; Conservative 21; Mismatches 73; Indels 40; Gaps 7;
QY 27 VEVFSETEAVGNPKMLKICSMKREVEAT--TVVWFYFPGKGDFL-IYEVNGHQ 82
Db 40 VYTFKEIFVANGQKGLTCKT---KFKSTSTTGLTSVMSFQPGADATTVSFPHSQGV 95
QY 83 EVES--PFQGLQKNSKDLQVSTVLNVLTNSGLYTCNVSREFEFAHRPPVKTEL 140
Db 96 YLGNVFPFQRIASHAGLDKQASININMNOFTNGTYICDVN----- 139
QY 141 IPLRVTEAGEDFTSVSE-----IMWILLVFLMLLIEMICY--RKVSKA 187
Db 140 -PDDVVGQGHIRYVVEKENLPFVFWVWVGIVTAVVLGLTLLISMLAVLYRNSKR 198
QY 188 E 188
Db 199 D 199

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RESULT 12
US-09-430-503-22
; Sequence 22, Application US/09430503
; Patent No. 6355786
; APPLICANT: ZHAO, Zhizhuang
; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND
; TITLE OF INVENTION: THERAPEUTIC AND SCREENING METHODS USING SAME
; FILE REFERENCE: Actonway Docket No. 6355786 1242-11/2
; CURRENT APPLICATION NUMBER: US/09/430,503

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; CURRENT FILING DATE: 1999-10-29
 ; NUMBER OF SEQ ID NOS: 49
 ; SOFTWARE: PatentIn Ver. 2.0
 ; LENGTH: 209
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-430-503-22

Query Match 11.38; Score 127; DB 4; Length 209;
 Best Local Similarity 36.08; Pred. No. 7.8e-06;
 Matches 47; Conservative 21; Mismatches 73; Indels 40; Gaps 7;
 QY 27 VVPSFEATVQGNPMKLCISCKMREVEAT---TVVWFTRFEGKGDFL-IYVENHQ 82
 DB 40 VYTFKEIFVANGTQKLC---AKFSSTTGCLTSVNSFQEGADTVSFFHQGV 95
 QY 83 EYES--PFQGLQNSGKQDQVITVAVLNDSGLYTCNVSRFEFAHPFVKTFL 140
 DB 96 YLGNVFPKRIISAGLDQKQDQVITVAVLNDSGLYTCNVSRFEFAHPFVKTFL 140
 QY 141 IFLAVTEAGDEFTVSE-----IMWLLVLTLLMLIEMVICY--RUKVA 187
 DB 140 -PDVIVQVQHILAVYVENKLVFPVFWVVGIVTAVVLGTLISLILAVIYRANR 198
 QY 188 E 188
 DB 199 D 199

RESULT 13
 US-09-430-503-24
 ; Sequence 24; Application US/09430503
 ; Title of Invention: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND
 ; GENERAL INFORMATION:
 ; APPLICANT: Zhao, Zhizhuang
 ; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND
 ; FILE REFERENCE: ATTORNEY DOCKET NO. 6355786 1242-11/2
 ; CURRENT APPLICATION NUMBER: US/09/430,503
 ; CURRENT FILING DATE: 1999-10-29
 ; NUMBER OF SEQ ID NOS: 49
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 24
 ; LENGTH: 209
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-430-503-24

Query Match 11.38; Score 127; DB 4; Length 209;
 Best Local Similarity 36.08; Pred. No. 7.8e-06;
 Matches 47; Conservative 21; Mismatches 73; Indels 40; Gaps 7;
 QY 27 VVPSFEATVQGNPMKLCISCKMREVEAT---TVVWFTRFEGKGDFL-IYVENHQ 82
 DB 40 VYTFKEIFVANGTQKLC---AKFSSTTGCLTSVNSFQEGADTVSFFHQGV 95
 QY 83 EYES--PFQGLQNSGKQDQVITVAVLNDSGLYTCNVSRFEFAHPFVKTFL 140
 DB 96 YLGNVFPKRIISAGLDQKQDQVITVAVLNDSGLYTCNVSRFEFAHPFVKTFL 140
 QY 141 IFLAVTEAGDEFTVSE-----IMWLLVLTLLMLIEMVICY--RUKVA 187
 DB 140 -PDVIVQVQHILAVYVENKLVFPVFWVVGIVTAVVLGTLISLILAVIYRANR 198
 QY 188 E 188
 DB 199 D 199

RESULT 14
 US-09-430-503-26
 ; Sequence 26; Application US/09430503

; Patent No. 6355786
 ; GENERAL INFORMATION:
 ; APPLICANT: Zhao, Zhizhuang
 ; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND
 ; FILE REFERENCE: ATTORNEY DOCKET NO. 6355786 1242-11/2
 ; CURRENT APPLICATION NUMBER: US/09/430,503
 ; CURRENT FILING DATE: 1999-10-29
 ; NUMBER OF SEQ ID NOS: 49
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 26
 ; LENGTH: 270
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-430-503-26

Query Match 11.18; Score 125; DB 4; Length 270;
 Best Local Similarity 36.08; Pred. No. 1.9e-05;
 Matches 47; Conservative 23; Mismatches 78; Indels 26; Gaps 8;
 QY 27 VVPSFEATVQGNPMKLCISCKMREVEAT---TVVWFTRFEGKGDFL-IYVENHQ 82
 DB 40 VYTFKEIFVANGTQKLC---AKFSSTTGCLTSVNSFQEGADTVSFFHQGV 95
 QY 83 EYES--PFQGLQNSGKQDQVITVAVLNDSGLYTCNVSRFEFAHPFVKTFL 134
 DB 96 YLGNVFPKRIISAGLDQKQDQVITVAVLNDSGLYTCNVSRFEFAHPFVKTFL 154
 QY 135 VYCTFLPLVTEAGDEFTVSEIMWLLVLTLLMLIEMVICYKVKSAE 188
 DB 155 VEIDMLVPLVNWVVG-TTVAVVLGTLISLILAVIYRANR 199

RESULT 15
 US-09-430-503-28
 ; Sequence 28; Application US/09430503
 ; Title of Invention: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND
 ; GENERAL INFORMATION:
 ; APPLICANT: Zhao, Zhizhuang
 ; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND
 ; FILE REFERENCE: ATTORNEY DOCKET NO. 6355786 1242-11/2
 ; CURRENT APPLICATION NUMBER: US/09/430,503
 ; CURRENT FILING DATE: 1999-10-29
 ; NUMBER OF SEQ ID NOS: 49
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 28
 ; LENGTH: 270
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-430-503-28

Query Match 11.18; Score 125; DB 4; Length 270;
 Best Local Similarity 27.04; Pred. No. 1.9e-05;
 Matches 47; Conservative 23; Mismatches 78; Indels 26; Gaps 8;
 QY 27 VVPSFEATVQGNPMKLCISCKMREVEAT---TVVWFTRFEGKGDFL-IYVENHQ 82
 DB 40 VYTFKEIFVANGTQKLC---AKFSSTTGCLTSVNSFQEGADTVSFFHQGV 95
 QY 83 EYES--PFQGLQNSGKQDQVITVAVLNDSGLYTCNVSRFEFAHPFVKTFL 134
 DB 96 YLGNVFPKRIISAGLDQKQDQVITVAVLNDSGLYTCNVSRFEFAHPFVKTFL 154
 QY 135 VYCTFLPLVTEAGDEFTVSEIMWLLVLTLLMLIEMVICYKVKSAE 188
 DB 155 VEIDMLVPLVNWVVG-TTVAVVLGTLISLILAVIYRANR 199

Search completed: December 5, 2003, 23:24:06
 Job time: 31 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 5, 2003, 23:10:38 (Search time 78 seconds
with 11 million cells)
512.647 Million cell updates/sec

Title: US-09-936-680-2

Perfect score: 1124

Sequence: 1 MWAFNRLPLASLVLIVWS.....SDYLAIFSNKSNKSNVPEE 215

Scoring table: BIOSUM62 Gap0 10.0, Gapext 0.5

Searched: 684280 seqs, 185983659 residues

Total number of hits satisfying chosen parameters: 684280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 10%

Listing first 45 summaries

Databases:

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/ECT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
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- 7: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1124	100.0	215	10	US-09-997-579-2
2	1124	100.0	215	15	US-10-142-2018-11
3	1105	98.3	215	14	US-10-029-191-2
4	1105	98.3	215	14	US-10-143-2018-12
5	1105	98.3	215	15	US-10-029-191-4
6	986	87.7	191	14	US-10-029-191-4
7	986	87.7	191	14	US-10-029-191-4
8	832	70.0	159	10	US-09-997-579-2
9	557	53.1	111	14	US-10-029-191-5
10	477	42.4	118	14	US-10-029-191-20
11	471	41.9	218	10	US-09-997-579-44
12	471	41.9	218	10	US-09-997-579-44
13	282	25.1	58	14	US-10-029-191-7
14	268.5	23.0	268	9	US-09-875-456A-14
15	207	18.4	39	10	US-09-997-579-17

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16 196 17.4 39 10 US-09-997-579-18
17 165 14.7 34 10 US-09-997-579-31
18 161 14.3 34 10 US-09-997-579-47
19 160.5 14.3 235 12 US-10-216-163-238
20 160.5 14.3 235 12 US-10-216-163-238
21 160.5 14.3 235 12 US-10-219-065-238
22 160.5 14.3 235 12 US-10-219-066-238
23 160.5 14.3 235 12 US-10-219-066-238
24 160.5 14.3 235 12 US-10-219-066-238
25 160.5 14.3 235 12 US-10-219-066-238
26 160.5 14.3 235 12 US-10-219-073-238
27 160.5 14.3 235 12 US-10-219-475-238
28 160.5 14.3 235 12 US-10-219-475-238
29 160.5 14.3 235 12 US-10-219-526-238
30 160.5 14.3 235 12 US-10-219-526-238
31 160.5 14.3 235 12 US-10-219-526-238
32 160.5 14.3 235 12 US-10-219-530-238
33 160.5 14.3 235 12 US-10-219-531-238
34 160.5 14.3 235 12 US-10-219-531-238
35 160.5 14.3 235 12 US-10-219-531-238
36 160.5 14.3 235 12 US-10-230-437-238
37 160.5 14.3 235 12 US-10-230-437-238
38 160.5 14.3 235 12 US-10-232-228-238
39 160.5 14.3 235 15 US-10-222-684-238
40 160.5 14.3 235 15 US-10-230-163-238
41 160.5 14.3 235 15 US-10-230-336-238
42 160.5 14.3 235 15 US-10-231-145-12
43 160.5 14.3 235 15 US-10-231-145-12
44 160.5 14.3 235 15 US-10-216-159A-238
45 160.5 14.3 235 15 US-10-216-159A-238

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ALIGNMENTS

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US-09-997-579-2
; Sequence 2, Application US/0997579
; APPLICATION INFORMATION: University Technical Services
; TITLE OF INVENTION: A novel family of beta sub-unit proteins from a voltage gated ion
; TITLE OF INVENTION: channel
; TITLE OF INVENTION: nucleic acids encoding them and therapeutic or diagnostic uses
; CURRENT APPLICATION NUMBER: US/09/997,579
; PRIOR APPLICATION NUMBER: ECT/EP00/01783
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: US/02/0129,473
; PRIOR FILING DATE: 2006-02-24
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NOS: Patentin version 3.1
; LENGTH: 215
; TYPE: PRT
; ORIGIN: Homo sapiens
US-09-997-579-2
Query Match
Best Local Similarity 100.0%; Score 1124; DB 10; Length 215;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 MWAFNRLPLASLVLIVWSVCFVVFSETRAVQNMPLKRICSKMRSEVATTVV 60
Db 1 MWAFNRLPLASLVLIVWSVCFVVFSETRAVQNMPLKRICSKMRSEVATTVV 60
Oy 61 EMFTPEEGGDFLIVETFGHGVSEPFQGRQNNKSDJQNSIVTAVYVNDLSGYTC 120
Db 61 EMFTPEEGGDFLIVETFGHGVSEPFQGRQNNKSDJQNSIVTAVYVNDLSGYTC 120
Oy 121 NVNSFEFARFVFKTLLPLVETEGAGQFVSFSEWMLLIVFVTLVNLKRYTC 180
Db 121 NVNSFEFARFVFKTLLPLVETEGAGQFVSFSEWMLLIVFVTLVNLKRYTC 180

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Db 121 NVSGFEFEHRRFFVKTLLPLAVTEAGEDFTSVSEIMWILLVPLTLLMLLEIMYC 180
Qy 181 YKYSKAEBAQENASDIATLPSNKENSAVPVEE 215
Db 181 YKYSKAEBAQENASDIATLPSNKENSAVPVEE 215

RESULT 2

US-10-142-2018-11
; Publication US/101422018
; Sequence 1, Application US/00220220541
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals Inc.
; TITLE OF INVENTION: A SODIUM CHANNEL BETA 4 SUBUNIT,
; FILE REFERENCE: MP12001-106FIN(M)
; CURRENT FILING DATE: 2002-05-09/142,2018
; PRIOR FILING DATE: 2002-05-09/142,2018
; PRIOR APPLICATION NUMBER: US 60/289,893
; SOFTWARE: SEQ ID NOS: 12
; SEQ ID NO 11: webseq for Windows Version 4.0
; LENGTH: 215
; ORGANISM: Homo sapiens
US-10-142-2018-11

Query Match 100.0%; Score 1124; DB 15; Length 215;
Best Local Similarity 98.1%; Pred. No. 1.3e-109;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPAFNPFLASLIVLVTVVSCFPCVCFVSTETAVQNPMLKRCISCKNKEVEATTV 60
Db 1 MPAFNPFLASLIVLVTVVSCFPCVCFVSTETAVQNPMLKRCISCKNKEVEATTV 60
Qy 61 EMFVPRGGKDFLTETNGHQVESEFPQRLQNSKQLOVSTVNTVNLNSGLYC 120
Db 61 EMFVPRGGKDFLTETNGHQVESEFPQRLQNSKQLOVSTVNTVNLNSGLYC 120
Qy 121 NVSGFEFEHRRFFVKTLLPLAVTEAGEDFTSVSEIMWILLVPLTLLMLLEIMYC 180
Db 121 NVSGFEFEHRRFFVKTLLPLAVTEAGEDFTSVSEIMWILLVPLTLLMLLEIMYC 180
Qy 181 YKYSKAEBAQENASDIATLPSNKENSAVPVEE 215
Db 181 YKYSKAEBAQENASDIATLPSNKENSAVPVEE 215

RESULT 3

US-09-997-579-1
; Publication US/09997579
; Patent No. US20020113203A1
; GENERAL INFORMATION:
; APPLICANT: Cambridge University Technical Services
; TITLE OF INVENTION: A channel family of beta sub-unit proteins from a voltage gated ion

; FILE REFERENCE: 674558-2001 US/09/997,579
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: PCT/EP00/01783
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60,129,473
; SOFTWARE: SEQ ID NOS: 47
; SEQ ID NO 1
; LENGTH: 215
; ORGANISM: Rat
US-09-997-579-1

Query Match 98.1%; Score 1105; DB 10; Length 215;
Best Local Similarity 98.1%; Pred. No. 1.3e-107;
Matches 211; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 MPAFNPFLASLIVLVTVVSCFPCVCFVSTETAVQNPMLKRCISCKNKEVEATTV 60
Db 1 MPAFNPFLASLIVLVTVVSCFPCVCFVSTETAVQNPMLKRCISCKNKEVEATTV 60
Qy 61 EMFVPRGGKDFLTETNGHQVESEFPQRLQNSKQLOVSTVNTVNLNSGLYC 120
Db 61 EMFVPRGGKDFLTETNGHQVESEFPQRLQNSKQLOVSTVNTVNLNSGLYC 120
Qy 121 NVSGFEFEHRRFFVKTLLPLAVTEAGEDFTSVSEIMWILLVPLTLLMLLEIMYC 180
Db 121 NVSGFEFEHRRFFVKTLLPLAVTEAGEDFTSVSEIMWILLVPLTLLMLLEIMYC 180
Qy 181 YKYSKAEBAQENASDIATLPSNKENSAVPVEE 215
Db 181 YKYSKAEBAQENASDIATLPSNKENSAVPVEE 215

RESULT 4

US-10-029-191-2
; Sequence 2, Application US/10029191
; Publication No. US20020160453A1
; GENERAL INFORMATION:
; APPLICANT: Rony A. J.
; TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT
; FILE REFERENCE: 210147.00XK/SU1
; CURRENT FILING DATE: 2003-11/US/029,191
; PRIOR APPLICATION NUMBER: 09/569,978
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/134,198
; SOFTWARE: SEQ ID NOS: 23
; SEQ ID NO 2
; LENGTH: 215
; ORGANISM: Rattus sp.
US-10-029-191-2

Query Match 98.1%; Score 1105; DB 14; Length 215;
Best Local Similarity 98.1%; Pred. No. 1.3e-107;
Matches 211; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Db 1 MPAFNPFLASLIVLVTVVSCFPCVCFVSTETAVQNPMLKRCISCKNKEVEATTV 60
Qy 61 EMFVPRGGKDFLTETNGHQVESEFPQRLQNSKQLOVSTVNTVNLNSGLYC 120
Db 61 EMFVPRGGKDFLTETNGHQVESEFPQRLQNSKQLOVSTVNTVNLNSGLYC 120
Qy 121 NVSGFEFEHRRFFVKTLLPLAVTEAGEDFTSVSEIMWILLVPLTLLMLLEIMYC 180
Db 121 NVSGFEFEHRRFFVKTLLPLAVTEAGEDFTSVSEIMWILLVPLTLLMLLEIMYC 180
Qy 181 YKYSKAEBAQENASDIATLPSNKENSAVPVEE 215
Db 181 YKYSKAEBAQENASDIATLPSNKENSAVPVEE 215

RESULT 5

US-10-142-2018-12
; Sequence 12, Application US/101422018
; Publication No. US20030022205A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals Inc.
; APPLICANT: Curtius, Roy A.J.

1 TITLE OF INVENTION: 98359, A SODIUM CHANNEL BETA 4 SUBUNIT,
2 TITLE OF INVENTION: AND USES THEREOF
3 TITLE OF INVENTION: A NOVEL FAMILY OF BETA SUB-UNIT PROTEINS FROM A VOLTAGE GATED SO
4 CURRENT APPLICATION NUMBER: US/10/142, 201B
5 CURRENT FILING DATE: 2002-05-09
6 PRIOR APPLICATION NUMBER: US 60/289,893
7 PRIOR FILING DATE: 2001-05-09
8 NUMBER OF SEQ ID NOS: 201-05-09
9 SOFTWARE: FastSeq for Windows Version 4.0
10 SEQ ID NO 12
11 LENGTH: 215
12 TYPE: PRT
13 ORGANISM: Rattus norvegicus
14 ORGANISM: Rattus norvegicus
15 US-10-142-201B-12

Query Match 98.31; Score 1105; DB 15; Length 215;
Best Local Similarity 98.31; Pred. No. 2.5e-80;
Matches 211; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 MPAFNRLPFLASLVLVWVVCPCVVEPSTEAVQGNPKMLCISCKQKREVEATVTV 60
DB 1 MPAFNRLPFLASLVLVWVVCPCVVEPSTEAVQGNPKMLCISCKQKREVEATVTV 60
QY 61 EWPYFREGKQPLLYETNGHQVSPFOQLQNGSKLOQVSTVLTNTLNSGLTYC 120
DB 61 EWPYFREGKQPLLYETNGHQVSPFOQLQNGSKLOQVSTVLTNTLNSGLTYC 120
QY 121 NVSRFEFFRANPFPVTRILPLVTRAGEDFTVVSIMVLTLLVLTLLLEMITYC 180
DB 121 NVSRFEFFRANPFPVTRILPLVTRAGEDFTVVSIMVLTLLVLTLLLEMITYC 180
QY 181 YKVSKEAEAAQNASDYLAIPEKNSKNSAVPVEE 215
DB 181 YKVSKEAEAAQNASDYLAIPEKNSKNSAVPVEE 215

Result 69-191-4
1 Sequence 4; Application US/10029191
2 Publication No. US20020160453A1
3 GENERAL INFORMATION: Accession No. 5
4 TITLE OF INVENTION: A NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT
5 TITLE OF INVENTION: PROTEIN
6 TITLE OF INVENTION: A NOVEL FAMILY OF BETA SUB-UNIT PROTEINS FROM A VOLTAGE GATED SO
7 CURRENT APPLICATION NUMBER: US/10/029,191
8 CURRENT FILING DATE: 2004-05-12
9 PRIOR APPLICATION NUMBER: 09/569,978
10 PRIOR FILING DATE: 2000-05-12
11 NUMBER OF SEQ ID NOS: 23
12 SOFTWARE: PatSeq In Ver. 2.1
13 SEQ ID NO 4
14 LENGTH: 231
15 TYPE: PRT
16 ORGANISM: Rattus sp.
17 US-10-029-191-4

Query Match 87.71; Score 986; DB 14; Length 191;
Best Local Similarity 99.04; Pred. No. 3.3e-95;
Matches 189; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 25 VCVEVFSTEAVQGNPKMLCISCKQKREVEATVTFREGKQPLLYETNGHQV 84
DB 1 VCVEVFSTEAVQGNPKMLCISCKQKREVEATVTFREGKQPLLYETNGHQV 84
QY 85 EWPYFREGKQPLLYETNGHQVSPFOQLQNGSKLOQVSTVLTNTLNSGLTYC 144
DB 61 EWPYFREGKQPLLYETNGHQVSPFOQLQNGSKLOQVSTVLTNTLNSGLTYC 120
QY 145 VTREAGDFTSVSEIMILLVLTLLVLTLLLEMITYCYNKSKAEAAQNASDYLAIPEE 204

Db 121 VTREAGDFTSVSEIMILLVLTLLVLTLLLEMITYCYNKSKAEAAQNASDYLAIPEE 180
QY 205 MENSAPVPER 215
Db 181 MENSAPVPER 191
RESULT 7
US-09-997-579-22
1 Sequence 22; Application US/09997579
2 Patent No. US20020113203A1
3 GENERAL INFORMATION: Accession No. 7
4 TITLE OF INVENTION: A NOVEL FAMILY OF BETA SUB-UNIT PROTEINS FROM A VOLTAGE GATED SO
5 TITLE OF INVENTION: channel
6 TITLE OF INVENTION: nucleic acids encoding then and therapeutic or diagnostic uses
7 CURRENT APPLICATION NUMBER: US/09/997,579
8 CURRENT FILING DATE: 2002-04-05
9 PRIOR APPLICATION NUMBER: ECT/EP00/01783
10 PRIOR FILING DATE: 2000-02-24
11 NUMBER OF SEQ ID NOS: 60, 129, 473
12 SOFTWARE: Patent in version 3.1
13 SEQ ID NO 159
14 LENGTH: 159
15 TYPE: PRT
16 ORGANISM: Homo sapiens
17 US-09-997-579-22

Query Match 75.04; Score 843; DB 10; Length 159;
Best Local Similarity 100.04; Pred. No. 2.5e-80;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPAFNRLPFLASLVLVWVVCPCVVEPSTEAVQGNPKMLCISCKQKREVEATVTV 60
DB 1 MPAFNRLPFLASLVLVWVVCPCVVEPSTEAVQGNPKMLCISCKQKREVEATVTV 60
QY 61 EWPYFREGKQPLLYETNGHQVSPFOQLQNGSKLOQVSTVLTNTLNSGLTYC 120
DB 61 EWPYFREGKQPLLYETNGHQVSPFOQLQNGSKLOQVSTVLTNTLNSGLTYC 120
QY 121 NVSRFEFFRANPFPVTRILPLVTRAGEDFTVVSIMVLTLLVLTLLLEMITYC 159
DB 121 NVSRFEFFRANPFPVTRILPLVTRAGEDFTVVSIMVLTLLVLTLLLEMITYC 159

Result 8
US-09-997-579-23
1 Sequence 23; Application US/09997579
2 Patent No. US20020113203A1
3 GENERAL INFORMATION: Accession No. 8
4 TITLE OF INVENTION: A NOVEL FAMILY OF BETA SUB-UNIT PROTEINS FROM A VOLTAGE GATED SO
5 TITLE OF INVENTION: channel
6 TITLE OF INVENTION: nucleic acids encoding then and therapeutic or diagnostic uses
7 CURRENT APPLICATION NUMBER: US/09/997,579
8 CURRENT FILING DATE: 2002-04-05
9 PRIOR APPLICATION NUMBER: ECT/EP00/01783
10 PRIOR FILING DATE: 2000-02-24
11 NUMBER OF SEQ ID NOS: 47
12 SOFTWARE: Patent in version 3.1
13 SEQ ID NO 23
14 LENGTH: 159
15 TYPE: PRT
16 ORGANISM: Homo sapiens
17 US-09-997-579-23

Query Match 74.04; Score 832; DB 10; Length 159;

Best Local Similarity 98.7%; Pred. No. 3,6e-79;
Matches 157; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MAFNRLFFPLASLLVWVSCFVCVCFVSETEAVQGNPMALACISCMKREVEATVWVFPRREG 60
Db 1 MAFNRLFFPLASLLVWVSCFVCVCFVSETEAVQGNPMALACISCMKREVEATVWVFPRREG 60
QY 61 SMYFPRREGDGLIYENRNGHVEESPQORLQNGSKDQVSTVLTAVTNGSLGYTC 120
Db 61 SMYFPRREGDGLIYENRNGHVEESPQORLQNGSKDQVSTVLTAVTNGSLGYTC 120
QY 121 NVSRGFEFPAHREFVMTLPLVETVETAGEDFTVSWSE 159
Db 121 NVSRGFEFPAHREFVMTLPLVETVETAGEDFTVSWSE 159

RESULT 9

QY 1029-191-5
; Sequence 5, Application US/10029191
; Publication No. US20020160431A1
; GENERAL INFORMATION: R05Y A.J.
; APPLICANT: Cambridge University Technical Services
; TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT
; FILE REFERENCE: 210147.000X/501
; CURRENT FILING DATE: 2001-10-20/US/029,191
; PRIOR APPLICATION NUMBER: 09/569,978
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/134,198
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ. ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ. ID NO 5
; TYPE: PRT
; ORGANISM: Rattus sp.
US-10-029-191-5

Query Match 53.1%; Score 597; DB 14; Length 111;
Best Local Similarity 100.0%; Pred. No. 9,2e-55;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 25 VCVVSEFTEAVQGNPMALACISCMKREVEATVWVFPRREGDGLIYENRNGHVE 84
Db 1 VCVVSEFTEAVQGNPMALACISCMKREVEATVWVFPRREGDGLIYENRNGHVE 84
QY 85 ESFQFQLQNGSKDQVSTVLTAVTNGSLGYTCVETVWVFPRREGDGLIYENRNGHVE 135
Db 61 ESFQFQLQNGSKDQVSTVLTAVTNGSLGYTCVETVWVFPRREGDGLIYENRNGHVE 135

RESULT 10

US-10-029-191-20
; Sequence 20, Application US/10029191
; Publication No. US20020160451A1
; GENERAL INFORMATION: R05Y A.J.
; APPLICANT: CURTIS, ROY A.J.
; TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT
; FILE REFERENCE: 210147.000X/501
; CURRENT FILING DATE: 2001-10-20/US/10/029,191
; PRIOR APPLICATION NUMBER: 09/569,978
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/134,198
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ. ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ. ID NO 11
; TYPE: PRT
; ORGANISM: Lepus sp.

US-10-029-191-20

Query Match 42.4%; Score 477; DB 14; Length 218;
Best Local Similarity 49.5%; Pred. No. 8,6e-42;
Matches 106; Conservative 32; Mismatches 68; Indels 8; Gaps 5;
QY 10 LASLVLVWVSCFVCVCFVSETEAVQGNPMALACISCMKREVEATVWVFPRREG 69
Db 10 LASLVLVWVSCFVCVCFVSETEAVQGNPMALACISCMKREVEATVWVFPRREG 69
QY 5 LAPFGVGLVSSAGCCVSEUSSEVYNTVFKLISCGRSETTATFTMTFRQGT 64
Db 5 LAPFGVGLVSSAGCCVSEUSSEVYNTVFKLISCGRSETTATFTMTFRQGT 64
QY 70 KDFL-1VEYNRNGHVEESP--FQGLRWNGS--KDLQDVSTVLTAVTNGSLGYTCWS 123
Db 70 KDFL-1VEYNRNGHVEESP--FQGLRWNGS--KDLQDVSTVLTAVTNGSLGYTCWS 123
QY 65 ESFQFQLYENRNGHVEESPQORLQNGSKDQVSTVLTAVTNGSLGYTCVCHY 124
Db 65 ESFQFQLYENRNGHVEESPQORLQNGSKDQVSTVLTAVTNGSLGYTCVCHY 124
QY 124 RESEFPAHREFVMTLPLVETVETAGEDFTVSWSEKMLLVLTAVTNGSLGYTCVK 183
Db 124 RESEFPAHREFVMTLPLVETVETAGEDFTVSWSEKMLLVLTAVTNGSLGYTCVK 183
QY 125 RLSPFENRHSVSKVHLVVDKARDMASTVSEMTAVTLVLTAVNABWYCTCK 184
Db 125 RLSPFENRHSVSKVHLVVDKARDMASTVSEMTAVTLVLTAVNABWYCTCK 184
QY 184 VSKA-EEAAGNADSLAIPSEKEN-SANVPER 215
Db 184 VSKA-EEAAGNADSLAIPSEKEN-SANVPER 215
QY 185 INAAETAAAGNASEYLAITSEKNCCTGVAAE 218
Db 185 INAAETAAAGNASEYLAITSEKNCCTGVAAE 218

RESULT 11

US-09-997-579-44
; Sequence 44, Application US/09997579
; Publication No. US200101203A1
; GENERAL INFORMATION: R05Y A.J.
; APPLICANT: Cambridge University Technical Services
; TITLE OF INVENTION: A novel family of beta sub-unit proteins from a voltage gated sc
; FILE REFERENCE: 674558-2001
; CURRENT FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: US/09/997,579
; PRIOR FILING DATE: 2000-02-24/EP00/01783
; PRIOR FILING DATE: 2000-02-24/EP00/01783
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ. ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ. ID NO 44
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-997-579-44

Query Match 42.0%; Score 472; DB 10; Length 218;
Best Local Similarity 49.1%; Pred. No. 2,9e-41;
Matches 105; Conservative 33; Mismatches 68; Indels 8; Gaps 5;
QY 10 LASLVLVWVSCFVCVCFVSETEAVQGNPMALACISCMKREVEATVWVFPRREG 69
Db 5 LAAPGVGLVSSAGCCVSEUSSEVYNTVFKLISCGRSETTATFTMTFRQGT 64
QY 70 KDFL-1VEYNRNGHVEESP--FQGLRWNGS--KDLQDVSTVLTAVTNGSLGYTCWS 123
Db 70 KDFL-1VEYNRNGHVEESP--FQGLRWNGS--KDLQDVSTVLTAVTNGSLGYTCWS 123
QY 65 ESFQFQLYENRNGHVEESPQORLQNGSKDQVSTVLTAVTNGSLGYTCVCHY 124
Db 65 ESFQFQLYENRNGHVEESPQORLQNGSKDQVSTVLTAVTNGSLGYTCVCHY 124
QY 124 RESEFPAHREFVMTLPLVETVETAGEDFTVSWSEKMLLVLTAVTNGSLGYTCVK 183
Db 124 RESEFPAHREFVMTLPLVETVETAGEDFTVSWSEKMLLVLTAVTNGSLGYTCVK 183
QY 184 VSKA-EEAAGNADSLAIPSEKEN-SANVPER 215
Db 184 VSKA-EEAAGNADSLAIPSEKEN-SANVPER 215
QY 185 INAAETAAAGNASEYLAITSEKNCCTGVAAE 218
Db 185 INAAETAAAGNASEYLAITSEKNCCTGVAAE 218

RESULT 12

US-10-145-2018-8
; Sequence 8, Application US/1014201B
; Publication No. US2003022105A1
; GENERAL INFORMATION:

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: APPLICANT: Millennium Pharmaceuticals Inc.
: TITLE OF INVENTION: 89159-A SODIUM CHANNEL BETA 4 SUBUNIT,
: FILE NO.: 89159-A (US) (P) (US) (P) (US) (P) (US) (P)
: FILE REFERENCE: WP12001-106P1SNW
: CURRENT APPLICATION NUMBER: US/10/142,201B
: CURRENT FILING DATE: 2002-05-09
: PRIOR FILING DATE: 2001-05-09
: NUMBER OF SEQ ID NOS: 12
: SOFTWARE: FastSBQ for Windows Version 4.0
: SEQ ID NO 1: 1
: SEQ ID NO 2: 8
: TYPE: PRT
: ORGANISM: Homo Sapiens
: US-10-142-201B-8
:
: Query Match 41.9%; Score 471; DB 15; Length 218;
: Best Local Similarity 49.5%; Pred. No. 3.7e-41;
: Matches 106; Conservative 61; Mismatches 49; Gaps 6;
:
: QY 10 LASLVLLVSVGFCVGVSESTVAGVQVWGLKSCSKEEVATVVFAPVDEGG 59
: D6 15 LAUQVALLVSSAGCGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGV 59
: QY 70 KPTL-LVYEVNGVSESP--FGQRLQVSG--VQDQVGVVLTAVTNGSLGVNYS 123
: QY 65 EBFVKLVLENVGLVDEEFEGFGRVWVNSGVGQVQDLSIFITVTVNSGVTECHY 124
: QY 124 REFEHSHRFVKTSLPLDVTEHAGCDGTSVGVSTVGVVLTAVTNGSLGVNYS 183
: QY 125 ALLFENVEHNTSVVKVHLHIVDFVQVKNAMSHVLSHVVLLVTLVAVKMYCYK 183
: QY 184 VSKA-EEAGGVGVVGVVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGV 218
: QY 185 IAAETTAGGASVYLAETSENGCTGVQVAB 218

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; Patent No. US20020045522A1
; GENERAL INFORMATION:
; APPLICANT: Oltz, Ning
; INVENTOR: Oltz, Ning
; ATTORNEY: Michael D'Audrea, Michael
; TITLE OF INVENTION: DNAs encoding human beta2a sodium channel subunit
; FILE REFERENCE: ORT-1221
; CURRENT APPLICATION NUMBER: US/09/875,456A
; PRIORITY DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; Length: 266
; TYPE: CDS
; ORGANISM: Homo sapiens
; US-09-875-456A-14

Query Watch      23.0%; Score 259.5; DB 9; Length 266;
Best Local Similarity 43.2%; Pred. No. 9,2e-19;
Matches 64; Conservative 20; Mismatches 57; Indels 7; Gaps 4;

Qy 10 LASALVLTWVSFCVPCVCFSTETANQGVHLCISGCGSEVFATTVIVKPVRSQC 69
Db | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 5 LALLVAAGLVSSACGGCVSDETFAYGTMLCLSCSGREINATFTMTFKNGT 64
Db | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 70 KDFL-IYYNNGHQEVSP--FGGLQQNS---KLQLGVITVLNTLMSGLYCNYS 123.
Db | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 124 REEFSEAFRRPFVKTRLPLAVTERAGE 151
Db | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 125 RLLEFFENYENTSVKKHLIEVDVK-GE 151
Db | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESUME 15
US-99-579-17
; Sequence 17, Application US/09957979
; Patent No. US20020113203A1
; GENERAL INFORMATION:
; APPLICANT: University Technical Services
; INVENTOR: novel family of beta sub-unit proteins from a voltage gated co
; TITLE OF INVENTION: channel
; TITLE OF INVENTION: nucleic acid encoding them and therapeutic or diagnostic uses
; FILE REFERENCE: 674558-2001
; CURRENT FILING DATE: 2002-04-05
; PRIOR FILING DATE: 2000-02-24
; PRIORITY DATE: 2000-02-24
; CURRENT FILING DATE: 2002-04-05
; PRIOR FILING DATE: 2000-02-24
; PRIORITY DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; Length: 107
; TYPE: CDS
; ORGANISM: homo sapiens
; US-09-997-579-17

Query Watch      18.4%; Score 207; DB 10; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.6e-14;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPANLPPLASLVLTIVWSVCVPCVCFSTETAVQN 39
Db | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1 MPANLPPLASLVLTIVWSVCVPCVCFSTETAVQN 39
Db | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Search completed: December 5, 2003, 23:25:16
Job time : 79 secs
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diagnostic uses these of
 HARMER-LAMBERT COMPANY (US) ; Cambridge University Technical
 Services Limited (GB)
 Location/Qualifiers
 source
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 263 a 386 c 372 g 260 t

Query Match 100.0%; Score 1261; db 6; Length 1261;
 Best Local Similarity 100.0%; From: 0; To: 0;
 Matches 1261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 C C C T C C T T C C G A G A G T T A C C T T G G C C C A A A G A G A G C G C G C G C G A G T G G 60

Qy 61 A A G C T G A G T C C C G G G G C G G G G A G G G G A G C T G C C G T G T G T G T G A C C G C G G A G A 120
 Db 61 A A G C T G A G T C C C G G G G C G G G G A G G G G A G C T G C C G T G T G T G T G A C C G C G G A G A 120

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 Db 121 G G G G G C G A G G C G G T A T G G G T C C C T C G A A C T G G G A G G T C C A G T G G G G T G C T T A G 180

Qy 181 G C C C A A A G C C C C A G C C C T C C A A A G C T C C C A G G C C C C C C A G G C C A C C G T G C G 240
 Db 181 G C C C A A A G C C C C A G C C C T C C A A A G C T C C C A G G C C C C C C A G G C C A C C G T G C G 240

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 Db 241 G C C T T T C C T G G T C A G A A G T G C C C C T G G G G G C A G T T G T C C A A A G G G T T C C T G C 300

Qy 301 A A A G A T C T G A G G G C A G C T C T G A C G A G G A G A T C T G T G T A G C T T G A G C 360
 Db 301 A A A G A T C T G A G G G C A G C T C T G A C G A G G A G A T C T G T G T A G C T T G A G C 360

Qy 361 C S C C A C C C C A G A G T G C T G C C T C A A T A G A T T G T T C C C G G C T C T C T G T G T T 420
 Db 361 C S C C A C C C C A G A G T G C T G C C T C A A T A G A T T G T T C C C G G C T C T C T G T G T T 420

Qy 421 A C T C T A T G G G T A G T G T C T C C T C C T C A T A G A T T G T T C C C G G C T C T C T G T G T T 480
 Db 421 A C T C T A T G G G T A G T G T C T C C T C C T C A T A G A T T G T T C C C G G C T C T C T G T G T T 480

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Qy 541 G C C A C C C G G G T G G T G C T C A G C G C 600
 Db 541 G C C A C C C G G G T G G T G C T C A G C G C 600

Qy 601 G A G T T G G G A T T G C 660
 Db 601 G A G T T G G G A T T G C 660

Qy 661 G A G T T G G G A T T G C 720
 Db 661 G A G T T G G G A T T G C 720

Qy 721 G C C T C T C A C C T C A A T G T G T C C C G A G T T T A G T T A G G G C C A T C C C C C T T T G G 780
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Qy 781 A A G A C A C C C C C C T G A T C C C C C T A G A G T C A C C A G G A G G C C T G A G A G A C T C A C C T 840
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Qy 841 G T G G T C T C A G A A T C A T G T A C A T C T T T G T G G T C T T C C T C C C A C C T G T G G C T A T C 900

841 G T G G T C T C A G A A T C A T G T A C A T C T T T G T G G T C T T C C A C C T G T G G C T A T C 900
 Qy 901 G A G A T A T A T T G C A T A G A T T C C A A G A G G T C C A A G A G G C C C C A G A A A C C G C 960
 Db 901 G A G A T A T A T T G C A T A G A G G T C C A A G A G G C C C C A G A A A C C G C 960

Qy 961 T T G A C T A C T T C C C A C C A T C C C A T C C A T C C A G A A G A A C T T C T T C A C T A G A A 1020
 Db 961 T T G A C T A C T T C C C A C C A T C C C A T C C A T C C A G A A G A A C T T C T T C A C T A G A A 1020

Qy 1021 T A G A C A G A G C G G T G A C A T G A G G T G C T G A C A C C T C G A G A C T G A C A C T C A T G 1080
 Db 1021 T A G A C A G A G C G G T G A C A T G A G G T G C T G A C A C C T C G A G A C T G A C A C T C A T G 1080

Qy 1081 T T G A C A G T C A T G C A T G A G G G C C C C A A G G G C C C A T C C T C C T C A T C G C 1140
 Db 1081 T T G A C A G T C A T G C A T G A G G G C C C C A A G G G C C C A T C C T C C T C A T C G C 1140

Qy 1141 A T C C A T T G T T G T C A T T C A T T C A T C A T C A C T C C C T T G A G C T T C A C C T C T 1200
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Qy 1201 G A C T C C T A A C T C A C A G A C T C A C G A C C A A G A G A C T C C C A G A C T G A A G C C 1260
 Db 1201 G A C T C C T A A C T C A C A G A C T C A C G A C C A A G A G A C T C C C A G A C T G A A G C C 1260

Qy 1261 G 1261
 Db 1261 G 1261

RESULT 2
 HS243396 1261 bp mRNA linear PRI 13-042-2000
 LOCUS HS243396
 DEFINITION Hs243396 mRNA for voltage-gated sodium channel beta-3 subunit.
 (scn3b gene).
 ACCESSION AJ243396.2 GI:7242612
 VERSION 1
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Morgan K., Stevens E.B., Shaw B., Cox P., Dixon A.K., Lee K.,
 Pincock R.D., Hughes J., Richardson P.J., Mizuguchi K. and
 Jackson A.P. Additional auxiliary subunit of the voltage-sensitive
 sodium channel that modulates channel gating with distinct kinetics
 Proc. Natl. Acad. Sci. U.S.A. 97 (5), 2308-2313 (2000)
 2010048
 REFERENCES 1 Morgan K.
 2 0686874
 3 Morgan K.
 Direct Submission
 Submitted (28-JUN-2000) Morgan K., Biochemistry, University of
 Cambridge, Tennis Court Road, Cambridge, CB2 1QW, UNITED KINGDOM
 Reversed by [4]
 (bases 1 to 1261)
 REFERENCE 3 Morgan K. Submission
 Submitted (13-MAR-2000) Morgan K., Biochemistry, University of
 Cambridge, Tennis Court Road, Cambridge, CB2 1QW, UNITED KINGDOM
 On Mar 14, 2000 this sequence version replaced gi:7160974.
 COMMENT
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 /organism="Homo sapiens"
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 /gene="scn3b"

gene

[illegible]

[illegible]


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* 21971 30780: contig of 8810 bp in length
* 30781 gap of unknown length
* 39268 39268: contig of 12664 bp in length
* 39268 39268: gap of unknown length
* 39368 46890: contig of 7523 bp in length
* 46891 46891: gap of unknown length
* 46891 46891: contig of 12664 bp in length
* 59557 59557: gap of unknown length
* 59557 83308: contig of 23553 bp in length
* 83309 83408: gap of unknown length
* 83409 83409: gap of unknown length
* 83310 111957: contig of 28448 bp in length
* 111958 111957: contig of 28448 bp in length
* 111958 144833: contig of 32876 bp in length.

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FEATURES

source

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BASE COUNT 38456 a 33920 c 34111 g 37093 t 1249 others
ORIGIN

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Matches 428; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CTCCTTCCTGAGCTTACCTTCGGCGCAACGACGAGCGAGGGCCGAGTGGA 42
Db 50353 CTCCTTCCTGAGCTTACCTTCGGCGCAACGACGAGCGAGGGCCGAGTGGA 50294
Qy 63 GCTGGAGTTCGCGGTGCGCGGAGCGAGCTGCTCGGTGCTGAGCCCGCGAGAGC 122
Db 50293 GCTGGAGTTCGCGGTGCGCGGAGCGAGCTGCTCGGTGCTGAGCCCGCGAGAGC 50234
Qy 123 GCGCGCGAGCGGCTGATCGCTCCCTCGAACTGGGAGGTCAGTGGGTCGCTAGGG 182
Db 50233 GCGCGCGAGCGGCTGATCGCTCCCTCGAACTGGGAGGTCAGTGGGTCGCTAGGG 50174
Qy 183 CCCAAGCCCGCCACCGGCTCCAAAGGTCCTCCAGGGGCTCCCGAGGACGGTGTGGC 242
Db 50173 CCCAAGCCCGCCACCGGCTCCAAAGGTCCTCCAGGGGCTCCCGAGGACGGTGTGGC 50114
Qy 243 CTTCTCTTCGTGAGAAAGTCGCGCTGGGGGAGTTCCTCCAAAGGGTTCTCGAA 102
Db 50113 CTTCTCTTCGTGAGAAAGTCGCGCTGGGGGAGTTCCTCCAAAGGGTTCTCGAA 50054
Qy 303 AGAATCTGAGAGGGGCGAGCTCTTGACCGAGGGAACTCTCTGTGTAGCTTGAGAGCC 362
Db 50053 AGAATCTGAGAGGGGCGAGCTCTTGACCGAGGGAACTCTCTGTGTAGCTTGAGAGCC 49994
Qy 363 CCAGCCCGCAAGATGCTGCTCAATAGATCTTCCTCCCTGCTCTCTCTGCTTAT 422
Db 49993 CCAGCCCGCAAGATGCTGCTCAATAGATCTTCCTCCCTGCTCTCTCTGCTTAT 49934
Qy 423 CTACTGGG 430
Db 49933 CTACTGGG 49926

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Job time : 5274.75 secs

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WPI; 2000-665241/64.
P-PSDB; AAB36002.

Novel nucleic acids encoding a beta-3 subunit from a voltage-gated sodium channel, and their corresponding polypeptides, useful for detecting and treating sodium channel-associated conditions, e.g. pain, epilepsy and stroke -

Claim 10: Page 70-71: 88pp: English.

The present sequence is given in the claims of a specification relating to a novel family of beta sub-unit proteins from a voltage-gated sodium channel. Human and rat beta sub-units, which are highly homologous, have been sequenced and compared. The polypeptides and polypeptides are useful for screening for agonists and antagonists of sodium channels. The agonists, antagonists and analogues of sodium channels may be used in the treatment of conditions associated with voltage-gated sodium channels, e.g. pain, epilepsy, atroke, ischemia, heart disease, Jacobson Syndrome, Familial Hemiplegic Migraine, Narcolepsy, Epilepsy, Multiple Sclerosis, Neurochondromatosis Paraganglioma, Phenylketonuria and Charcot Tooth

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 Matches 1261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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ABA93727;

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DT 30-APR-2002 (first entry)

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XX Human; foetal brain; foetal kidney; melanoma; testis; amygdala;
 KW gene therapy; ss.

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OS Homo sapiens.XX
PN
NO200198454-A2.XX
PD 27-DEC-2001.

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PF
25-APR-2001: 2001WO-IB02050.

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PR 25-APR-2000: 2000HS-199380P.

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PA (GEHU-) GERMAN HUMAN GENOME PROJECT.XX
PT
Wiemann S.

WPI: 2002-055860/07

DB 213 CTACGACCAATGAGTCTGCAAGCACTGAGGC 246
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RESULT 15

AB017864

AB017864 standard; DNA, 4625 BP.

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21.

Human testicular antigen encoding DNA fragment

SQ ID NO: 2516.

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21.

Human testicular antigen encoding DNA fragment

SQ ID NO: 2516.

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PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249266.
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 PR 17-NOV-2000; 2000US-0249269.
 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250161.
 PR 01-DEC-2000; 2000US-0251031.
 PR 01-DEC-2000; 2000US-0251032.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 05-DEC-2000; 2000US-0256720.
 PR 05-DEC-2000; 2000US-0256721.
 PR 05-DEC-2000; 2000US-0251852.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251870.
 PR 08-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JUN-2001; 2001US-0259678.
 PR
 PR (HUMA-) HUMAN GENOME SCI INC.
 PR
 PR Rosen CA, Barash SC, Ruben SM;
 PR WPI; 2001-48323/52.
 PR
 PR Nucleic acids encoding 973 human testicular antigen polypeptides,
 PR useful for preventing, diagnosing and/or treating testicular cancer -
 PR
 PR Disclosure; SEQ ID NO 2516; 766bp; English.
 PR
 PR The present invention provides the protein and coding sequences of 973
 PR human testicular antigen polypeptides. The protein and coding sequences
 PR of the human testicular antigen polypeptides can be used in the treatment of
 PR the reproductive system, immune, respiratory, neurological, urinary system,
 PR gastrointestinal disorders, infections, and particularly cancer.
 PR The present invention also provides a protein and coding sequence of a
 PR protein fragment of the invention.
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 DB 33 AGTGTGCTTGAACACTGAGGACTGAGACATCCCATGTTGACCAATGTCATGCGCATCG 92
 QY 1104 GAGGCGCCGCCAAGGCGCCCATCGCTTCCTTCATCATCATCATGTTGTTGTTATCAT 1163
 DB 93 GAGGCGCCGCCAAGGCGCCCATCGCTTCCTTCATCATCATCATGTTGTTGTTATCAT 152
 QY 1164 CAT 1223
 DB 153 CAT 212
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 DB 213 CTACCCACCATGAGCTCTCCGAGACTGAGAGCC 248

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Job time : 479.25 secs

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THE UNIVERSITY OF CHICAGO

1 APPLICATION NUMBER: US 08/790,462
 2 TITLE: ENZYME INFORMATION:
 3 ATTORNEY/AGENT INFORMATION:
 4 NAME: D. Douglas Price
 5 REGISTRATION NUMBER: 24,514
 6 FILING DATE: 05/19/95
 7 TELECOMMUNICATION INFORMATION:
 8 TELEPHONE: (202) 638-6666
 9 TELEFAX: (202) 39505350
 10 INFORMATION FOR SEQ ID NO: 20:
 11 LENGTH: 1669 base pairs
 12 STRANDEDNESS: single
 13 TOPOLOGY: linear
 14 MOLECULE TYPE: DNA (genomic)
 15 US-09-385-028-20

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 Best Local Similarity 47.4%; Pred. No. 3-7; Mismatches 121; Indels 0; Gaps 0;

Matches 109; Conservative 0; Mismatches 121; Indels 0; Gaps 0;

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QY 678 GAGAGTGTCTATCTGCTCAAGCTCATCTGAGAGCTGTGCTCTCACTGCA 737
 DB 1110 GAGAGGCGCTCCCGGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 1169

QY 738 TGTGTCTGCGAGGTGAGTTGAGGCGATGCGGCTTTTGAGAGAGAGCGGCTGAT 797
 DB 1170 GCGCGCTCCGAGAGCGCTGAGAGAGCTGAGAGAGCTGAGAGAGCTGAGAGAGCT 1229

QY 798 CCCCCCTAGAGTCCAGAGAGCTGAGAGAGCTTCACTCTGTGCT 847
 DB 1230 CCCCCGCGTGGCGATCGAGGAGTGTGAGCTTCCCTGCGGCACT 1279

RESULT 5

US-09-726-614-20

Application US/09726614

Patent No. 6314735

GENERAL INFORMATION:

APPLICANT: Susan E. Jensen

INVENTOR: Susan E. Jensen

APPLICANT: Ashleigh S. Paraskar

TITLE OF INVENTION: DNA Sequence Encoding Enzymes of Clavulanic

Patent No. 6314735

INVENTOR: Susan E. Jensen

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: JACOBSON, PRICE, HOLMAN & STERN, PLLC

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/726,614

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/790,462

ATTORNEY/AGENT INFORMATION:

NAME: D. Douglas Price

REGISTRATION NUMBER: 24,514

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 638-6666

1 REGISTRATION NUMBER: 24,514
 2 TITLE: ENZYME INFORMATION:
 3 ATTORNEY/AGENT INFORMATION:
 4 NAME: D. Douglas Price
 5 REGISTRATION NUMBER: 24,514
 6 FILING DATE: 05/19/95
 7 TELECOMMUNICATION INFORMATION:
 8 TELEPHONE: (202) 638-6666
 9 TELEFAX: (202) 39505350
 10 INFORMATION FOR SEQ ID NO: 20:
 11 LENGTH: 1669 base pairs
 12 STRANDEDNESS: single
 13 TOPOLOGY: linear
 14 MOLECULE TYPE: DNA (genomic)
 15 US-09-726-614-20

Query Match 2.9%; Score 36.4; DB 4; Length 1669;
 Best Local Similarity 47.4%; Pred. No. 3-7; Indels 0; Gaps 0;

Matches 109; Conservative 0; Mismatches 121; Indels 0; Gaps 0;

QY 618 CAGAGAGTGGAGAGCCCTTTCAGAGGCGCTCTGAGTGAATGAGAGAGAGCTGCA 677
 DB 1050 CTTGACGCGTGTACAGACCTTTCAGAGGCGCTCTGAGTGAATGAGAGAGAGCTGCA 1109

QY 678 GAGAGTGTCTATCTGCTCAAGCTCATCTGAGAGCTGTGCTCTCACTGCA 737
 DB 1110 GAGAGGCGCTCCCGGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 1169

QY 738 TGTGTCTGCGAGGTGAGTTGAGGCGATGCGGCTTTTGAGAGAGAGCGGCTGAT 797
 DB 1170 GCGCGCTCCGAGAGCGCTGAGAGAGCTGAGAGAGCTGAGAGAGCTGAGAGAGCT 1229

QY 798 CCCCCCTAGAGTCCAGAGAGCTGAGAGAGCTTCACTCTGTGCT 847
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RESULT 6

US-09-385-028-13

Application US/09385028

Patent No. 6232106

GENERAL INFORMATION:

APPLICANT: Susan E. Jensen

INVENTOR: Susan E. Jensen

APPLICANT: Ashleigh S. Paraskar

TITLE OF INVENTION: DNA Sequence Encoding Enzymes of Clavulanic

Patent No. 632106

INVENTOR: Susan E. Jensen

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: JACOBSON, PRICE, HOLMAN & STERN, PLLC

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/385,028

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/790,462

ATTORNEY/AGENT INFORMATION:

NAME: D. Douglas Price

REGISTRATION NUMBER: 24,514

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 638-6666

TELEFAX: (202) 39305350
 INFORMATION: RCN 248593 IDEA UR
 INFORMATION: RCN 248593 IDEA UR
 SEQUENCE CHARACTERISTICS:
 LENGTH: 11604 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-09-385-028-13

Query Match 2.9%; Score 36.4; DB 3; Length 11604;
 Best Local Similarity 47.4%; Pred. No. 7.4; Indels 0; Gaps 0;
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 QY 618 CCGAGAGGTGGAGAGCCCTTCAGGGGCGCTCGAGTGAAGTGCAGAGAGACTGCA 677
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 DB 8318 GAGAGCGCGCGCCCGGCGGCTGAGTCTGCGAGTCTGCGGACCGGCTTCGCACACGAT 8377
 QY 738 TGTGTCGCGAGGATTTGATTTGTGAGGGGATCGGCGCTTGTGAGAGAGCGGCGTGT 797
 DB 8378 GCGCCCGCGGAGAGACCGCGCTGAGAGTACCGGCGTGCAGAGCGCTGCGCCCGCGCT 8437
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RESULT 7
 US-09-726-614-13
 Sequence 1, Application US/09726614
 Patent No. 6514735
 GENERAL INFORMATION:
 APPLICANT: Susan E. Jensen
 APPLICANT: Ashish S. Parashar
 APPLICANT: Ashish S. Parashar
 TITLE OF INVENTION: DNA Sequence Encoding Enzymes of Clavulanic
 Patent No. 6514735 ON: Acid Biosynthesis
 NUMBER OF SEQUENCES: 25
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: JACOBSON, PRICE, HOLMAN & STERN, PFLC
 STREET: The Jenner Building, 400 Seventh Street, N.W.
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20004
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
 CURRENT APPLICATION NUMBER: US/09/726, 614
 FILING DATE:
 PRIORITY DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/790, 462
 FILING DATE: 29-JAN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: D. Douglas Price
 REGISTRATION NUMBER: 24,514
 REFERENCE/DOCKET NUMBER: 1418/P57452052
 TELEPHONE: (202) 638-6666
 TELEFAX: (202) 39305350
 INFORMATION: RCN 248593 IDEA UR
 INFORMATION: RCN 248593 IDEA UR
 SEQUENCE CHARACTERISTICS:
 LENGTH: 11604 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

LENGTH: 11604 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-09-726-614-13

Query Match 2.9%; Score 36.4; DB 4; Length 11604;
 Best Local Similarity 47.4%; Pred. No. 7.4; Indels 0; Gaps 0;
 Matches 109; Conservative 0; Mismatches 121;
 QY 618 CCGAGAGGTGGAGAGCCCTTCAGGGGCGCTCGAGTGAAGTGCAGAGAGACTGCA 677
 DB 8258 CTTGCAAGCGCTCAAGAGCACTTCGCGCTACCGGCTGCGCCCGAGGACACCGGCACT 8317
 QY 678 GAGAGTGTCTCATCTGCTCAAGTCTCTGAGAGTCTGTGCTCTCACTCTGCA 737
 DB 8318 GAGAGCGCGCGCCCGGCGGCTGAGTCTGCGAGTCTGCGGACCGGCTTCGCACACGAT 8377
 QY 738 TGTGTCGCGAGGATTTGATTTGTGAGGGGATCGGCGCTTGTGAGAGAGCGGCGTGT 797
 DB 8378 GCGCCCGCGGAGAGACCGCGCTGAGAGTACCGGCGTGCAGAGCGCTGCGCCCGCGCT 8437
 QY 798 CCCCCCTAGAGTACCGAGAGCTGAGAGGACTCTCACTCTGTGTCT 847
 DB 8438 GCGCCCGGCTGCGCTCATCGAGCGAGGCTGTGAGACTTCCGTCGCGGCACT 8487

RESULT 8
 US-09-385-028-1
 Sequence 1, Application US/09385028
 Patent No. 6231106
 GENERAL INFORMATION:
 APPLICANT: Susan E. Jensen
 APPLICANT: Ashish S. Parashar
 APPLICANT: Ashish S. Parashar
 TITLE OF INVENTION: DNA Sequence Encoding Enzymes of Clavulanic
 Patent No. 6231106 ON: Acid Biosynthesis
 NUMBER OF SEQUENCES: 25
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: JACOBSON, PRICE, HOLMAN & STERN, PFLC
 STREET: The Jenner Building, 400 Seventh Street, N.W.
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20004
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/385, 028
 FILING DATE:
 PRIORITY DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/790, 462
 FILING DATE: 29-JAN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: D. Douglas Price
 REGISTRATION NUMBER: 24,514
 REFERENCE/DOCKET NUMBER: 1418/P57452052
 TELEPHONE: (202) 638-6666
 TELEFAX: (202) 39305350
 INFORMATION: RCN 248593 IDEA UR
 INFORMATION: RCN 248593 IDEA UR
 SEQUENCE CHARACTERISTICS:
 LENGTH: 11604 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

100

Db 3333 CACGCGCGCTCTCGGGAACTCCGAGATCCGCTCCCTCCGCGCGACGACGCGCA 3274
Qy 213 CAGGAGCTCTCCCGAGCACCAGGCTCTGCTCTCTTCTGCTGAGAACTGCGCTCTG 272
Db 3273 CAGGCTCTCGGCGAGCGACCCGACCTGGCGAGGCGGAGCCTATGCCGAGTCCGAC 3214
Qy 273 GGGCAGTTCTGCTCCGAAAGGCTTCTCTGAAAGATCTGAGAGGCGCAGTCTTTGACGA 332
Db 3213 CAGTCTGTTGTAAGGCTACCGGCTCCGCTACCGGAGCTCGCTCGTCTGCTCTGCTG 3154
Qy 333 GGAATCTCTCTGCTAGCTTGGAGCGCGCGCGACGCGCGCA 373
Db 3153 CAGCGCTCTCTCCGCGAG 3113

Search completed: December 5, 2003, 22:59:14
SDB time : 116 secs

Qy 181 GGCCCAAGAGCCGACCGCTCCAAAGGCTCCCGGGCTCCCAAGCAGCGTCTCTCG 240
 Db 181 GGCCCAAGAGCCGACCGCTCCAAAGGCTCCCGGGCTCCCAAGCAGCGTCTCTCG 240
 Qy 241 GCGCT 300
 Db 241 GCGCT 300
 Qy 301 AAG 360
 Db 301 AAG 360
 Qy 361 GCGCAG 420
 Db 361 GCGCAG 420
 Qy 421 ATTACTGAGTCT 480
 Db 421 ATTACTGAGTCT 480
 Qy 481 GTCTGAGTCT 540
 Db 481 GTCTGAGTCT 540
 Qy 541 GCGCAG 600
 Db 541 GCGCAG 600
 Qy 601 GAGTCTGAGTCT 660
 Db 601 GAGTCTGAGTCT 660
 Qy 661 GCGCAG 720
 Db 661 GCGCAG 720
 Qy 721 GCGTCTGAGTCT 780
 Db 721 GCGTCTGAGTCT 780
 Qy 781 AAG 840
 Db 781 AAG 840
 Qy 841 GTGCTGAGTCT 900
 Db 841 GTGCTGAGTCT 900
 Qy 901 GAGTCTGAGTCT 960
 Db 901 GAGTCTGAGTCT 960
 Qy 961 TGTGCTGAGTCT 1020
 Db 961 TGTGCTGAGTCT 1020
 Qy 1021 TAAAG 1080
 Db 1021 TAAAG 1080
 Qy 1081 TTGAG 1140
 Db 1081 TTGAG 1140
 Qy 1141 ATCTGAGTCT 1200
 Db 1141 ATCTGAGTCT 1200
 Qy 1201 GACTCTTAACT 1260
 Db 1201 GACTCTTAACT 1260

Qy 1261 G 1261
 Db 1261 G 1261

RESULTS 2

US-10-028-191-22
 ; Sequence 22, Application US/10029191
 ; Publication No. US20020160453A1
 ; GENE: PROTEIN
 ; APPLICATION: CDPTS, POY A.J.
 ; TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT
 ; TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT
 ; CURRENT FILING DATE: 2001-12-20
 ; PRIOR FILING DATE: 2000-05-12
 ; PRIOR FILING DATE: 1999-05-24
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 2
 ; LENGTH: 2632
 ; TYPE: DNA
 ; ORGANISM: Rattus sp.
 ; US-10-029-191-22

Query Match 44.4%; Score 559.6; DB 13; Length 2632;
 Best Local Similarity 84.4%; Pred. No. 3,8e-160;
 Matches 655; Conservative 0; Mismatches 114; Indels 7; Gaps 2;

Qy 371 AGAAGATCCCTCCCTCAATAGATGTTCCCTCCCTCTCTCTCTCTCTCTCTCTCT 430
 Db 371 AAGAGATCCCTCCCTCAATAGATGTTCCCTCCCTCTCTCTCTCTCTCTCTCTCT 430
 Qy 431 TGAGTCT 490
 Db 431 TGAGTCT 490
 Qy 491 ACCCATGAGTCT 550
 Db 491 ACCCATGAGTCT 550
 Qy 551 TGTGAGTCT 610
 Db 551 TGTGAGTCT 610
 Qy 611 ATGSCACAG 670
 Db 611 ATGSCACAG 670
 Qy 671 ACTCTGAG 730
 Db 671 ACTCTGAG 730
 Qy 731 CTGCAAGTCT 790
 Db 731 CTGCAAGTCT 790
 Qy 791 GCGTATCCCT 850
 Db 791 GCGTATCCCT 850
 Qy 851 AATCTGAG 910
 Db 851 AATCTGAG 910
 Qy 911 ATGTCAG 970
 Db 911 ATGTCAG 970
 Qy 971 TTGCT 1030
 Db 971 TTGCT 1030

718 CATGATGTGCTTCACGAGAGTTTCGAATTCGAGGACACACAGCGCTTTTGTGAACACACA 777
 Qy 791 GGTGATATGCTGCTGATGATACACGAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 850
 Db 778 GATCTATACCTTTCGATATCACTGAAGAGCGGAGAGAGCTTACCTTCGCTGGTCTCG 837
 Qy 851 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 910
 Db 838 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 897
 Qy 911 ATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 970
 Db 912 ATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 957
 Qy 971 TTGCTATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1022
 Db 958 TTGCTATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1009

RESULT 5

US-10-029-191-21
 ; Sequence 21, Application US/10029191
 ; Publication No. US20020160433A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CURTIS, RORY A. J.
 ; TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT
 ; TITLE OF INVENTION: PROTEIN
 ; CURRENT APPLICATION NUMBER: US/10/029,191
 ; PRIOR FILING DATE: 2001-12-20
 ; PRIOR APPLICATION NUMBER: 09/569,978
 ; PRIOR FILING DATE: 2000-05-12
 ; PRIOR APPLICATION NUMBER: US 60/134,198
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: Patent in Ver. 2.1
 ; LENGTH: 645
 ; TYPE: DNA
 ; ORGANISM: Rattus sp.
 ; BEST LOCAL SIMILARITY: 42.4%; Score 534.6; DB 13; Length 645;
 ; MATCHES 576; Conservative 0; Mismatches 69; Indels 0; Gaps 0;
 ; US-10-029-191-21

Query Match 42.4%; Score 534.6; DB 13; Length 645;
 Best Local Similarity 42.4%; Pred. No. 4.2e-55; Matches 576; Conservative 0; Mismatches 69; Indels 0; Gaps 0;
 Qy 376 ATGCT 435
 Db 1 ATGCT 60
 Qy 436 GTGCT 495
 Db 61 GTGCT 120
 Qy 496 ATGCT 555
 Db 121 ATGCT 180
 Qy 556 GAATGCT 615
 Db 118 GAATGCT 240
 Qy 616 CACGAGAGGAG 675
 Db 241 CACGAGAGGAG 300
 Qy 676 CAGGAG 735
 Db 301 CAGGAG 360
 Qy 736 ATGCT 795
 Db 361 ATGCT 420

Qy 796 ATGCT 855
 Db 421 ATGCT 480
 Qy 856 ATGCT 915
 Db 481 ATGCT 540
 Qy 916 ATGCT 975
 Db 541 ATGCT 600
 Qy 976 ATGCT 1020
 Db 601 ATGCT 645

RESULT 6

US-09-764-891-7659
 ; Sequence 7659, Application US/09764891
 ; Publication No. US20030077808A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CURTIS, RORY A. J.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: PC006
 ; CURRENT APPLICATION NUMBER: US/09/764,891
 ; PRIOR FILING DATE: 2001-12-20
 ; PRIOR APPLICATION DATA REMOVED - consult PALM or file wrapper
 ; NUMBER OF SEQ ID NOS: 10211
 ; SOFTWARE: Patent in Ver. 2.0
 ; LENGTH: 4623
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; BEST LOCAL SIMILARITY: 17.1%; Score 216; DB 11; Length 4623;
 ; MATCHES 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 ; US-09-764-891-7659

Query Match 17.1%; Score 216; DB 11; Length 4623;
 Best Local Similarity 100.0%; Pred. No. 4.2e-55; Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1044 AGTGTGCT 1103
 Db 33 AGTGTGCT 92
 Qy 1104 GAGGCGGCG 1163
 Db 93 GAGGCGGCG 152
 Qy 1164 CATCTATACATACATACATACATACATACATACATACATACATACATACATACATACATACAT 1223
 Db 153 CATCTATACATACATACATACATACATACATACATACATACATACATACATACATACATACAT 212
 Qy 1224 CTAGGAGCATAGAGCTCTGACAGACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1259
 Db 213 CTAGGAGCATAGAGCTCTGACAGACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 248

RESULT 7

US-10-029-191-23
 ; Sequence 23, Application US/10029191
 ; Publication No. US20020160433A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CURTIS, RORY A. J.
 ; TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT
 ; TITLE OF INVENTION: PROTEIN
 ; CURRENT APPLICATION NUMBER: US/10/029,191
 ; PRIOR FILING DATE: 2001-12-20
 ; PRIOR APPLICATION NUMBER: 09/569,978
 ; PRIOR FILING DATE: 2000-05-12
 ; PRIOR APPLICATION NUMBER: US 60/134,198
 ; PRIOR FILING DATE: 1999-05-14

/ NUMBER OF SEQ ID NOS: 23
/ BEST LOCAL SIMILARITY 57.7%; Pred. No. 16-34;
/ SEQ ID NO 2: Patentin Ver. 2.1
/ LENGTH: 657
/ TYPE: DNA
/ ORGANISM: Lepus Sp.
US-10-029-191-23

Query Match 11.8%; Score 148.2; DB 13; Length 657;
Best Local Similarity 57.7%; Pred. No. 16-34;
Matches 337; Conservative 0; Mismatches 229; Indels 21; Gaps 3;

QY 451 TGTGTGGAGTGGCCCTCGAGACGAGCGCGTCGAGGCGACACCCCATGAGCTGCGTCG 510
DB 61 TGTGTGGAGTGGCCCTCGAGACGAGCGCGTCGAGGCGACACCCCATGAGCTGCGTCG 120
QY 511 ATCTCTGTCGATGAGAGAGAGAGGTCGAGGCGACACCCCATGAGCTGCGTCGTCAC 570
DB 121 ATCTCTGTCGATGAGAGAGAGAGGTCGAGGCGACACCCCATGAGCTGCGTCGTCAC 570
QY 571 CCCGAGGCGGTGAAGATT-----TCTTATTATGAGTATCCGATGCGACACG 621
DB 181 CAGAGAGACCTGAGTGGTGTGTCGATCTCTGCGCTTGTGAGAGAGAGTGTCTGCG 240
QY 622 GAGTGAGAGACCCCTCTTCAGGCGCGCTCGACGTGAGTGGCGAG-----CAGAGC 672
DB 241 GAGAGAGAGACCGCTCTTCAGGCGCGCTCGACGTGAGTGGCGAG-----CAGAGC 300
QY 673 CTCGAGAGTGTCTCTCACTCTGTCGATGAGTGTCTGTCGATGAGTGTCTCTCACT 732
DB 301 CTCGAGAGTGTCTCTCACTCTGTCGATGAGTGTCTGTCGATGAGTGTCTCTCACT 360
QY 733 TGCATGTGTCTCGCGAGTGTCTGTCGATGAGTGTCTGTCGATGAGTGTCTCTCACT 792
DB 361 TGCATGTGTCTCGCGAGTGTCTGTCGATGAGTGTCTGTCGATGAGTGTCTCTCACT 420
QY 793 CTCGAGAGTGTCTCTCACTCTGTCGATGAGTGTCTGTCGATGAGTGTCTCTCACT 852
DB 431 AAGATCACTCTGAGGTGTGTGTCGATGAGTGTCTGTCGATGAGTGTCTCTCACT 480
QY 853 ATCTGATGATGATCT 912
DB 481 ATCTGATGATGATCT 540
QY 913 TGTCTGAGAGTGTCTCTCACTCTGTCGATGAGTGTCTGTCGATGAGTGTCTCTCACT 969
DB 541 TGTCTGAGAGTGTCTCTCACTCTGTCGATGAGTGTCTGTCGATGAGTGTCTCTCACT 600
QY 970 CTCGATGATGATCT 1006
DB 601 TTGCGCTCATCTCTGAGAGAGAGAGTCTCTGCG 637

RESULT 9

US-09-917-800A-1654
; Sequence 1654, Application US/09917800A
; Patent No. US20020119462A1
; GENERAL INFORMATION:
; APPLICANT: Dompe
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Rory
; APPLICANT: Castle, Arthur
; APPLICANT: Johnson, Michael
; APPLICANT: Gane Louis, Jr.
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5038-US
; PRIORITY CLAIM: US-09-917,800A
; CURRENT PILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 60/222,040
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 60/222,880
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 60/290,029

/ PRIOR FILING DATE: 2001-05-11
/ PRIOR APPLICATION NUMBER: US 60/290,645
/ PRIOR FILING DATE: 2001-05-15
/ PRIOR APPLICATION NUMBER: US 60/292,336
/ PRIOR FILING DATE: 2001-05-22
/ PRIOR APPLICATION NUMBER: US 60/295,798
/ PRIOR FILING DATE: 2001-06-06
/ PRIOR APPLICATION NUMBER: US 60/297,457
/ PRIOR FILING DATE: 2001-06-23
/ PRIOR APPLICATION NUMBER: US 60/298,884
/ PRIOR FILING DATE: 2001-06-19
/ PRIOR APPLICATION NUMBER: US 60/303,459
/ PRIOR FILING DATE: 2001-07-05
/ NUMBER OF SEQ ID NOS: 1740
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 1654
/ LENGTH: 1490
/ TYPE: DNA
/ ORGANISM: Rattus norvegicus
/ FEATURE: INFORMATION: Genbank Accession No. US20020119462A1 NM_017888
US-09-917-800A-1654

Query Match 11.0%; Score 138.6; DB 10; Length 1490;
Best Local Similarity 56.7%; Pred. No. 1.2e-31;
Matches 327; Conservative 0; Mismatches 229; Indels 21; Gaps 3;

QY 451 TGTGTGGAGTGGCCCTCGAGACGAGCGCGTCGAGGCGACACCCCATGAGCTGCGTCG 510
DB 280 TGTGTGGAGTGGCCCTCGAGACGAGCGCGTCGAGGCGACACCCCATGAGCTGCGTCG 339
QY 511 ATCTCTGTCGATGAGAGAGAGAGGTCGAGGCGACACCCCATGAGCTGCGTCGTCACG 570
DB 340 ATCTCTGTCGATGAGAGAGAGGTCGAGGCGACACCCCATGAGCTGCGTCGTCACG 399
QY 571 CCCGAGGCGGTGAAGATT-----TCTTATTATGAGTATCCGATGCGACACG 621
DB 400 CAGAGAGACCTGAGTGGTGTGTCGATCTCTGCGCTTGTGAGAGAGTGTCTGCGAG 459
QY 622 GAGTGAGAGACCCCTCTTCAGGCGCGCTCGACGTGAGTGGCGAG-----CAGAGC 672
DB 460 GAGAGAGTGTCTCTCACTCTGTCGATGAGTGTCTGTCGATGAGTGTCTCTCACT 732
QY 673 CTCGAGAGTGTCTCTCACTCTGTCGATGAGTGTCTGTCGATGAGTGTCTCTCACT 792
DB 520 CTCGAGAGTGTCTCTCACTCTGTCGATGAGTGTCTGTCGATGAGTGTCTCTCACT 579
QY 733 TGCATGTGTCTCGCGAGTGTCTGTCGATGAGTGTCTGTCGATGAGTGTCTCTCACT 792
DB 580 TGCATGTGTCTCGCGAGTGTCTGTCGATGAGTGTCTGTCGATGAGTGTCTCTCACT 639
QY 793 CTCGATGATGATCT 852
DB 640 AAGATCACTCTGAGGTGTGTGTCGATGAGTGTCTGTCGATGAGTGTCTCTCACT 699
QY 853 ATCTGATGATGATCT 912
DB 700 ATCTGATGATGATCT 759
QY 913 TGTCTGAGAGTGTCTCTCACTCTGTCGATGAGTGTCTGTCGATGAGTGTCTCTCACT 969
DB 760 TGTCTGAGAGTGTCTCTCACTCTGTCGATGAGTGTCTGTCGATGAGTGTCTCTCACT 819
QY 970 CTCGATGATGATCT 1006
DB 820 TTGCGCTCATCTCTGAGAGAGAGAGTCTCTGCG 856

RESULT 9

US-10-029-386-16214
; Sequence 16214, Application US/10029386
; Patent No. US2003019470A1
; GENERAL INFORMATION:


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1 FEATURE:
2 NAME/KEY: modified_base
3 LOCATION: (415)..(417)
4 OTHER INFORMATION: a, t, c, g, unknown or other
5 FEATURE:
6 NAME/KEY: modified_base
7 LOCATION: (415)..(417)
8 OTHER INFORMATION: a, t, c, g, unknown or other
9 FEATURE:
10 NAME/KEY: modified_base
11 LOCATION: (417)
12 OTHER INFORMATION: a, t, c, g, unknown or other
13 FEATURE:
14 NAME/KEY: modified_base
15 LOCATION: (417)
16 OTHER INFORMATION: a, t, c, g, unknown or other
17 NAME/KEY: modified_base
18 LOCATION: (415)
19 OTHER INFORMATION: a, t, c, g, unknown or other
20 NAME/KEY: modified_base
21 LOCATION: (311)
22 OTHER INFORMATION: a, t, c, g, unknown or other
23 NAME/KEY: modified_base
24 LOCATION: (322)
25 OTHER INFORMATION: a, t, c, g, unknown or other
26 NAME/KEY: modified_base
27 LOCATION: (326)
28 OTHER INFORMATION: a, t, c, g, unknown or other
29 NAME/KEY: modified_base
30 LOCATION: (345)..(349)
31 OTHER INFORMATION: a, t, c, g, unknown or other
32 NAME/KEY: modified_base
33 LOCATION: (351)..(361)
34 OTHER INFORMATION: a, t, c, g, unknown or other
35 FEATURE:
36 NAME/KEY: modified_base
37 LOCATION: (364)
38 OTHER INFORMATION: a, t, c, g, unknown or other
39 NAME/KEY: modified_base
40 LOCATION: (365)..(366)
41 OTHER INFORMATION: a, t, c, g, unknown or other
42 FEATURE:
43 NAME/KEY: modified_base
44 LOCATION: (360)
45 OTHER INFORMATION: a, t, c, g, unknown or other
46 FEATURE:
47 NAME/KEY: modified_base
48 LOCATION: (364)
49 OTHER INFORMATION: a, t, c, g, unknown or other
50 NAME/KEY: modified_base
51 LOCATION: (392)
52 OTHER INFORMATION: a, t, c, g, unknown or other
53 NAME/KEY: modified_base
54 LOCATION: (394)..(396)
55 OTHER INFORMATION: a, t, c, g, unknown or other
56 NAME/KEY: modified_base
57 LOCATION: (403)
58 OTHER INFORMATION: a, t, c, g, unknown or other
59 NAME/KEY: modified_base
60 LOCATION: (413)
61 OTHER INFORMATION: a, t, c, g, unknown or other
62 FEATURE:

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2 LOCATION: (415)..(417)
3 OTHER INFORMATION: a, t, c, g, unknown or other
4 NAME/KEY: modified_base
5 LOCATION: (422)
6 OTHER INFORMATION: a, t, c, g, unknown or other
7 NAME/KEY: modified_base
8 LOCATION: (438)..(439)
9 OTHER INFORMATION: a, t, c, g, unknown or other
10 FEATURE:
11 NAME/KEY: modified_base
12 LOCATION: (441)
13 OTHER INFORMATION: a, t, c, g, unknown or other
14 FEATURE:
15 NAME/KEY: modified_base
16 LOCATION: (441)
17 OTHER INFORMATION: a, t, c, g, unknown or other
18 NAME/KEY: modified_base
19 LOCATION: (441)
20 OTHER INFORMATION: a, t, c, g, unknown or other
21 NAME/KEY: modified_base
22 LOCATION: (445)
23 OTHER INFORMATION: a, t, c, g, unknown or other
24 NAME/KEY: modified_base
25 LOCATION: (449)..(471)
26 OTHER INFORMATION: a, t, c, g, unknown or other
27 FEATURE:
28 NAME/KEY: modified_base
29 LOCATION: (487)..(488)
30 OTHER INFORMATION: a, t, c, g, unknown or other
31 NAME/KEY: modified_base
32 LOCATION: (490)..(491)
33 OTHER INFORMATION: a, t, c, g, unknown or other
34 NAME/KEY: modified_base
35 LOCATION: (495)
36 OTHER INFORMATION: a, t, c, g, unknown or other
37 NAME/KEY: modified_base
38 LOCATION: (497)..(498)
39 OTHER INFORMATION: a, t, c, g, unknown or other
40 NAME/KEY: modified_base
41 LOCATION: (501)..(505)
42 OTHER INFORMATION: a, t, c, g, unknown or other
43 FEATURE:
44 NAME/KEY: modified_base
45 LOCATION: (519)
46 OTHER INFORMATION: a, t, c, g, unknown or other
47 NAME/KEY: modified_base
48 LOCATION: (523)..(530)
49 OTHER INFORMATION: a, t, c, g, unknown or other
50 FEATURE:
51 NAME/KEY: modified_base
52 LOCATION: (541)
53 OTHER INFORMATION: a, t, c, g, unknown or other
54 NAME/KEY: modified_base
55 LOCATION: (541)
56 OTHER INFORMATION: a, t, c, g, unknown or other
57 NAME/KEY: modified_base
58 LOCATION: (564)..(568)
59 OTHER INFORMATION: a, t, c, g, unknown or other
60 NAME/KEY: modified_base

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QY 203 CCAAAAGCTCCAGGGGCTCCCGAG 227
 Db 747 CTTGATGTGGGACCCCGAGCTG 771

RESULT 15

US-10-134-102-3
 ; Sequence 3, Application US/10134102
 ; Publication No. US20030186254A1
 ; Inventor: Moritz, Michael B.
 ; APPLICANT: Moritz, Michael B.
 ; APPLICANT: Moritz, Albrecht
 ; APPLICANT: Comb, Michael J.
 ; INVENTION: Regulation of HIV-Tat and Nef by the Pak1 kinase and its
 ; TITLE OF INVENTION: Identifying Partners and Methods of Identifying Modulators Thereof.
 ; FILE REFERENCE: GST-176 CIP
 ; CURRENT APPLICATION NUMBER: US/10/134,102
 ; CURRENT FILING DATE: 2002-04-29
 ; PRIOR FILING DATE: 2001-05/750,457
 ; PRIOR APPLICATION NUMBER: 60/173,939
 ; PRIOR FILING DATE: 1999-12-30
 ; SOURCE OF SEQ ID NOS: 10
 ; SOFTWARE: PatentIn ver. 2.0
 ; SEQ ID NO 3 PatentIn ver. 2.0
 ; LENGTH: 2838
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (211)..(1986)
 US-10-134-102-3

Query Match 3.2%; Score 40.2; DB 12; Length 2838;
 Best Local Similarity 49.8%; Pred. No. 0.17;
 Matches 102; Conservative 0; Mismatches 103; Indels 0; Gaps 0;
 QY 23 ACCCTGGGCGCCAAAGCGAGCGAGCGGGCGGAGTGGAGCTGGAGTTCCTGGGGTGGGC 82
 Db 577 ACCACGCGCCAGGGGGCGCCAGGAGAGCGAGCGAGCGAGCGCGGCTTCGCGCGTCAAGC 636
 QY 83 GGGAGCGCGACTGTCTCGGTGTGTGAGCTCCGCGCGAGCGCGCGCGCGCGCTGTATCG 142
 Db 637 GAGCGCGGTGTGGCGGACGTGTGTACACGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 696
 QY 143 GCTCCCTCGAACTGGGGAGGTTCAGTGGGGTCTTATGGGCGCGCGCGCGCGCGCGCG 202
 Db 697 TCGAGGAGAGGCGCTTGAGGGGGTCTCCCGAGAGTCTTCGCGCGCGCGCGCGCGCGCG 756
 QY 203 CCAAAAGCTCCAGGGGCTCCCGAG 227
 Db 757 CTTGATGTGGGACCCCGAGCTG 781

Search completed: December 5, 2003, 23:16:59
 Job time : 531 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 5, 2003, 14:16:11 ; Search time 2705.05 Seconds
Alignment algorithm: 9757.95 Million cell updates/sec

Title: US-09-936-680-4_COPY_376_1023

Perfect score: 648

Sequence: 1 aagctgccttaacagatt.....cgtaccagcggaggaatag 648

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 2888711 seqs, 2045481336 residues

Total number of hits satisfying chosen parameters: 577422

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database :

GenBank:
1: gb_ba:
2: gb_hg:
3: gb_in:
4: gb_mus:
5: gb_ov:
6: gb_pat:
7: gb_ph:
8: gb_pi:
9: gb_ro:
10: gb_ro:
11: gb_sts:
12: gb_yr:
13: gb_vl:
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15: em_ba:
16: em_fun:
17: em_hu:
18: em_in:
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31: em_hg_inv:
32: em_hg_other:
33: em_hg_mus:
34: em_hg_ov:
35: em_hg_rod:
36: em_hg_mam:
37: em_hg_vrt:
38: em_hg_hum:
39: em_hgo_hum:
40: em_hgo_hum:
41: em_hgo_other:

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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5	646.4	99.8	5006	9 AB0232984	AX039100 Homo sapi
6	517.2	82.9	5770	10 AX040436	AX039100 Mus muscu
7	536.6	82.8	2220	6 AX039099	AX039099 Sequence
8	536.6	82.8	2220	10 XM0243395	AX039099 Rattus no
9	536.6	82.8	2220	10 XM0243395	AX039099 Rattus no
10	536.6	82.8	3107	10 AX078093	AX039099 Rattus no
11	536.6	82.8	3107	10 AX078093	AX039099 Rattus no
12	534.6	82.5	645	6 AX048004	AX047984 Sequence
13	534.6	82.5	645	6 AX048004	AX048004 Sequence
14	534.6	82.5	12747	2 AF000682	AX048004 Homo sapi
15	529.6	35.4	172546	2 AC024604	AX040662 Homo sapi
16	229.6	35.4	176169	9 AF002765	AX024604 Homo sapi
17	229.6	35.4	176169	9 AF002765	AX024604 Homo sapi
18	229.6	35.4	176169	9 AF002765	AX024604 Homo sapi
19	228	35.2	144833	2 AC063921	AC063921 Homo sapi
20	228	35.2	149800	2 AC063921	AC063921 Homo sapi
21	147.9	27.6	24326	2 AC013981	AC013981 Homo sapi
22	147.9	27.6	24326	2 AC013981	AC013981 Rattus no
23	167.8	25.9	144833	2 AC063921	AC063921 Homo sapi
24	148.2	22.9	657	4 OC05382	AC063921 Homo sapi
25	148.2	22.9	657	4 OC05382	AC063921 Homo sapi
26	148.2	22.9	657	4 OC05382	AC063921 Homo sapi
27	143.8	22.2	1335	9 HUM0596	U05788 Mus musculu
28	138.6	21.4	1340	10 XM035786	U05788 Mus musculu
29	138.6	21.4	1340	10 XM035786	U05788 Mus musculu
30	138.6	21.4	1340	10 XM035786	U05788 Mus musculu
31	138.6	21.4	1340	10 XM035786	U05788 Mus musculu
32	138.6	21.4	1557	10 BC039140	BC039140 Homo sapi
33	138.6	21.4	1557	10 BC039140	BC039140 Homo sapi
34	138.6	21.4	1557	10 BC039140	BC039140 Homo sapi
35	138.6	21.4	1557	10 BC039140	BC039140 Homo sapi
36	81.4	12.6	807	6 AX354520	AX354520 Sequence
37	81.4	12.6	807	6 AX354520	AX354520 Sequence
38	74.4	11.5	13892	5 AX054521	AX054521 Sequence
39	74.4	11.5	13892	5 AX054521	AX054521 Sequence
40	73	11.3	850	6 AX111728	AX111728 Sequence
41	73	11.3	850	6 AX111728	AX111728 Sequence
42	64	9.9	178431	2 AF002766	AF002766 Rattus no
43	64	9.9	178431	2 AF002766	AF002766 Rattus no
44	55	8.5	66980	2 AC013796	AC013796 Homo sapi
45	55	8.5	149800	2 AC021981	AC021981 Homo sapi

ALIGNMENTS

Result	Score	Match	Length	DB ID	Description
1	648	100.0	1261	AX039100	Sequence
2	648	100.0	1261	AX039100	Sequence
3	646.4	99.8	4052	9 HS8443396	AX039100 Homo sapi
4	646.4	99.8	5006	9 AB0232984	AX039100 Homo sapi
5	646.4	99.8	5006	9 AB0232984	AX039100 Homo sapi
6	517.2	82.9	5770	10 AX040436	AX039100 Mus muscu
7	536.6	82.8	2220	6 AX039099	AX039099 Sequence
8	536.6	82.8	2220	10 XM0243395	AX039099 Rattus no
9	536.6	82.8	2220	10 XM0243395	AX039099 Rattus no
10	536.6	82.8	3107	10 AX078093	AX039099 Rattus no
11	536.6	82.8	3107	10 AX078093	AX039099 Rattus no
12	534.6	82.5	645	6 AX048004	AX047984 Sequence
13	534.6	82.5	645	6 AX048004	AX048004 Sequence
14	534.6	82.5	12747	2 AF000682	AX048004 Homo sapi
15	529.6	35.4	172546	2 AC024604	AX040662 Homo sapi
16	229.6	35.4	176169	9 AF002765	AX024604 Homo sapi
17	229.6	35.4	176169	9 AF002765	AX024604 Homo sapi
18	229.6	35.4	176169	9 AF002765	AX024604 Homo sapi
19	228	35.2	144833	2 AC063921	AC063921 Homo sapi
20	228	35.2	149800	2 AC063921	AC063921 Homo sapi
21	147.9	27.6	24326	2 AC013981	AC013981 Homo sapi
22	147.9	27.6	24326	2 AC013981	AC013981 Rattus no
23	167.8	25.9	144833	2 AC063921	AC063921 Homo sapi
24	148.2	22.9	657	4 OC05382	AC063921 Homo sapi
25	148.2	22.9	657	4 OC05382	AC063921 Homo sapi
26	148.2	22.9	657	4 OC05382	AC063921 Homo sapi
27	143.8	22.2	1335	9 HUM0596	U05788 Mus musculu
28	138.6	21.4	1340	10 XM035786	U05788 Mus musculu
29	138.6	21.4	1340	10 XM035786	U05788 Mus musculu
30	138.6	21.4	1340	10 XM035786	U05788 Mus musculu
31	138.6	21.4	1340	10 XM035786	U05788 Mus musculu
32	138.6	21.4	1557	10 BC039140	BC039140 Homo sapi
33	138.6	21.4	1557	10 BC039140	BC039140 Homo sapi
34	138.6	21.4	1557	10 BC039140	BC039140 Homo sapi
35	138.6	21.4	1557	10 BC039140	BC039140 Homo sapi
36	81.4	12.6	807	6 AX354520	AX354520 Sequence
37	81.4	12.6	807	6 AX354520	AX354520 Sequence
38	74.4	11.5	13892	5 AX054521	AX054521 Sequence
39	74.4	11.5	13892	5 AX054521	AX054521 Sequence
40	73	11.3	850	6 AX111728	AX111728 Sequence
41	73	11.3	850	6 AX111728	AX111728 Sequence
42	64	9.9	178431	2 AF002766	AF002766 Rattus no
43	64	9.9	178431	2 AF002766	AF002766 Rattus no
44	55	8.5	66980	2 AC013796	AC013796 Homo sapi
45	55	8.5	149800	2 AC021981	AC021981 Homo sapi

Pred. No. is the number of results predicted by chance to have a


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SOURCE          Lepus sp.
ORGANISM        Lepus sp.
REFERENCE        Buiakova, Metaxoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS          Mammalia; Eutheria; Lagomorpha; Leporidae; Lepus.
TITLE            Gene encoding a sodium channel beta-3 subunit protein
JOURNAL          Currie, R.A.
JOURNAL          Millennium Pharmaceuticals, Inc. (US)
FEATURES         Location/Qualifiers
source           1...645
                 /loc_type="transcript"
                 /db_xref="taxon:137772"
BASE COUNT      155 a 154 c 181 g 155 t
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Best Local Similarity 89.3%; Pred. No. 1.6e-115;
Matches 576; Conservative 0; Mismatches 69; Indels 0; Gaps 0;
QY 1 ATGCTGCGCTCAATGATGTTTCCCTGGCTCTCTCTGCTATCTACTGAGTCAGT 60
DB 1 ATGCTGCGCTCAACAGATGCTTCCCTAGCTCTCTAGTGTCTCATCTACTGGTGA 60
QY 61 GTCGTCTTCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 120
DB 61 GTCGTCTTCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 120
QY 121 ATGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 180
DB 121 ATGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 180
QY 181 GATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240
DB 181 GATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240
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DB 241 CACAGAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 300
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QY 541 TCAAGAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600
DB 541 TCAAGAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600
QY 601 ATCTCTCTCAAGAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 645
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RESULT 13
BD059018      471 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION    BD059018 expressed sequence tags (ESTs).
ACCESSION     BD059018.1 G1:22604624
VERSION        BD059018.1
KEYWORDS      JP 2001519666-A/873.

SOURCE          Zea mays
ORGANISM        Zea mays
REFERENCE        Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
AUTHORS          Spermatophyta; Monocotyledon; Liliopsida; Poales; Poaceae; PACAD
TITLE            clade; Panicoideae; Andropogoneae; Zea.
JOURNAL          1 (bases 1 to 471)
JOURNAL          Jacobo, K., McCoy, J. M., Lavallie, E. R., Racie, L. A., Merberg, D.,
JOURNAL          Patents: JP 2001519666-A 873 23-OCT-2001;
JOURNAL          GENETICS INSTITUTE INC
JOURNAL          PN 23-OCT-2001
JOURNAL          PF 10-APR-1998 JP 1998543068
JOURNAL          PF 10-APR-1997 US 08/835513
JOURNAL          PI KENNETH JACOB, JOHN M MCCOY, EDWARD R LAVALLIE, LISA A RACIE, PI
JOURNAL          PI MAURICE TERRY, VIKKI SPALDING, MICHAEL J AGOSTINO PC
JOURNAL          C12N15/12, C12N5/10, C07K14/47, C12Q1/68, A61K38/17 CC Strandedness:
JOURNAL          Double;
JOURNAL          CC Topology: Linear;
JOURNAL          FN Key Location/Qualifiers.
JOURNAL          source           1..471
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BASE COUNT      93 a 136 c 143 g 108 t 1 others
ORIGIN
Query Match     65.1%; Score 422; DB 6; Length 471;
Best Local Similarity 99.5%; Pred. No. 5.8e-89;
Matches 433; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 1 ATGCTGCGCTCAATGATGTTTCCCTGGCTCTCTCTGCTATCTACTGAGTCAGT 60
DB 1 ATGCTGCGCTCAATGATGTTTCCCTGGCTCTCTCTGCTATCTACTGAGTCAGT 60
QY 61 GTCGTCTTCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 120
DB 61 GTCGTCTTCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 120
QY 121 ATGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 180
DB 121 ATGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 180
QY 148 ATGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 207
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DB 181 GATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240
QY 208 GATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 267
DB 208 GATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 267
QY 241 CACAGAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 300
DB 241 CACAGAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 300
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DB 301 CAGAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
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DB 328 CAGAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 387
QY 361 ATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
DB 361 ATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
QY 388 ATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 447
DB 388 ATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 447
QY 421 ATCTCTCTCAAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 482
DB 421 ATCTCTCTCAAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 482

RESULT 14
AP000682/c
DEFINITION    AP000682 Home sapiens chromosome 11 clone OM9-32A1 map 11q24, WORKING DRAFT
ACCESSION     AP000682
KEYWORDS

```


GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 5, 2003, 14:12:31 ; Search time 244.092 Seconds
7166.298 Million cell updates/sec

Title: us-09-936-680-4_COPY_376_1023

Sequence: 1 atgccttcctcaatgatt.....cggaccacgtgggaatg 648

Scoring table: IDENTITY_NWC Gapop 10.0, Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 10%

Maximum Match 10%

Listing first 45 summaries

Database : N_Geneseq_1349603_*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	646	100.0	1261	21 AAC57837	Human betas3 cdna
2	646.4	99.8	1510	22 AAF84146	Human betas3 cdna
3	646.4	99.8	4052	24 ABA93727	Human signal trans
4	579.5	90.3	1045	22 AAC52345	Human polynucleoti
5	536.6	82.8	1045	22 AAC57836	Human betas3 subunit
6	536.6	82.8	2632	22 AAC29602	Rat sodium channel
7	536.6	82.8	3108	22 AAC29600	Rat sodium channel

9	534.8	82.5	1195	23 AAS86764	DNA encoding novel
10	534.6	82.5	645	22 AAC90601	Rat sodium channel
11	422	65.1	3511	23 AAS86763	EST clone BM4.10
12	392.6	60.6	3511	23 AAS86763	DNA encoding novel
13	234.4	34.6	621	23 AAS86762	Rabbit sodium chan
14	149.2	22.9	1657	22 AAC90603	Rabbit sodium chan
15	142.2	21.9	1414	25 ABZ32837	Human voltage-gate
16	141	21.8	407	22 ABA08942	Human polynucleoti
17	141	21.8	1490	22 AAS53329	Human polynucleoti
18	138.6	21.4	974	24 ABE33747	Rat sequence diffe
19	81.4	12.6	974	24 AAD29222	Human betas3 subu
20	73.3	11.3	850	22 AAF57672	Human betas3 subu
21	73.3	11.3	850	22 AAF30669	Rat sodium channel
22	47	7.3	509	22 AA193385	Sodium channel bet
23	45.4	7.0	1645	21 AAB88951	Human polynucleoti
24	42.2	6.5	5700	21 AAB78169	Maize geranylgeran
25	39.2	6.0	5973	24 AAS78752	DNA encoding novel
26	39.2	6.0	6202	25 ABE70893	Novel human cdna s
27	39.2	6.0	7584	25 ABZ36402	Novel human cdna s
28	38.8	6.0	1299	23 AB110133	Human secretory po
29	38.8	6.0	1299	23 AB110133	Drosophila melanog
30	38.6	6.0	1299	23 AB110133	Drosophila melanog
31	38.6	6.0	1179	23 AAS54061	Pseudomonas aerugi
32	38.6	6.0	2453	23 AB124082	Drosophila melanog
33	38.6	6.0	4166	23 AB124084	Drosophila melanog
34	37.8	5.9	1323	21 AAB78169	DNA encoding novel
35	37.8	5.9	1323	21 AAB78169	Drosophila melanog
36	37.4	5.8	6217	24 AB122939	Human immune syste
37	37.2	5.7	721	22 AAB08615	Human cdna clone (
38	37.2	5.7	1642	22 AAB16770	Human cdna sequenc
39	37.2	5.7	1642	22 AAB16770	Human cdna sequenc
40	37	5.7	12276	23 AB136374	Drosophila melanog
41	37	5.7	1558	22 AAF76859	Human secreted pro
42	36.6	5.6	1548	22 ABA07722	Human ovarian and
43	36.6	5.6	1548	22 ABA07722	Human reproductive
44	36.6	5.6	1548	22 ABA07722	Human immune/basoa
45	36.6	5.6	4583	23 AB128304	Drosophila melanog
46	36.6	5.6	6712	23 AB110229	Drosophila melanog

ALIGNMENTS

RESULT 1
AC67837
ID AAC67837 standard; cdna; 1261 bp.

XX AC AAC67837;

DT 15-FEB-2001 (first entry)

XX Human betas3 cdna.

Human betas3 sub-unit; betas; analgesic; anticonvulsant;
cerebroprotective; vasotropic; cardiac; notropic; cytostatic;
dermatological; gene therapy; voltage-gated sodium channel; pain;
epilepsy; stroke; ischemia; heart disease; Jacobson Syndrome;
Charcot-Marie-Tooth disease; Charcot-Marie-Tooth disease; 88.

OS Homo sapiens.

PX NC_0020063167.AL

PD 26-OCT-2000.

XX 24-FEB-2000; 2000W0-EPI01783.

PR 15-APR-1999; 99US-0129473.

XX (MORV) MANHEE LAMBERT CO.

PA (UTCA) UNIV CAMBRIDGE TECH SERVICES LTD.

XX Cox P, Dixon A, Jackson A, Morgan K;

PI

CONFIDENTIAL, BY AGREEMENT OF AMERICAN OVERSIGHT

CONFIDENTIAL, BY AGREEMENT OF AMERICAN OVERSIGHT

CONFIDENTIAL, BY AGREEMENT OF AMERICAN OVERSIGHT

CC animals, although no supporting data is given. Suggested activities
 CC include nutritional activity, immune stimulating or suppressing activity,
 CC hematopoietic activity, tissue growth activity, hematopoietic
 CC and thrombolytic activity, receptor/ligand activity, anti-inflammatory
 CC activity, cadherin/tumour invasion/suppressor activity, tumour inhibition
 CC activity. The EST sequences are also stated to be useful for gene
 CC therapy.

XX Sequence 471 BP; 93 A; 126 C; 143 G; 108 T; 1 other;

Query Match 55.1%; Score 422; DB 20; Length 471;
 Best Local Similarity 99.5%; P: N: 1.3e-11;
 Matches 433; Conservative 0; Mismatches 1; Gaps 1;
 QY 1 ATGCGCTCTTATATGATTTCTTCTGCTCTATCTACTGCTAGT 60
 DB 29 ATGCGCTCTTATATGATTTCTTCTGCTCTATCTACTGCTAGT 88
 QY 61 GTCTGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
 DB 69 GTCTGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 147
 QY 121 ATGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
 DB 148 ATGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 207
 QY 181 GAATGCTTCTACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
 DB 208 GAATGCTTCTACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 267
 QY 241 CACGAGAGGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
 DB 268 CACGAGAGGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 327
 QY 301 CAGGAGGTGCTCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
 DB 328 CAGGAGGTGCTCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 387
 QY 361 AATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
 DB 388 AATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 447
 QY 421 ATCCCTCTAAGATGC 435
 DB 448 ATCCCTCTAAGATGC 462

RESULT 12

AAS86763

XX AAS86763 standard; cDNA; 3531 BP.

XX AAS86763;

AC AAS86763;

XX 13-FEB-2002 (first entry)

DE DNA encoding novel human diagnostic protein #22567.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;

XX food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX Homo sapiens.

OS WO2001/7067-A2.

XX 11-OCT-2001.

PD 11-OCT-2001.

XX 30-MAR-2001; 2001MO-US08631.

XX 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649157.

XX (HYPE-) HY80 INC.

XX

PI Dmanac XT, Liu C, Tang YT;

XX WPI, 2001-43062/73.

XX P-FDDB; AS822576.

XX

PI New isolated polynucleotide and encoded polypeptides, useful in
 PI diagnostic, forensic, gene mapping, identification of mutations
 PI for genetic disorders or other traits and to assess
 PI biodiversity

XX Claim 1; SEQ ID NO 22567; 103pp; English.

XX

CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridization probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotide (I) is useful as a probe for identifying disease tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving or
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC a food supplement, polypeptide binding, as molecular weight markers and as
 CC a tool for studying the binding of (II) to (I). (I) and (II) are useful for
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS4197-AAS94564 represent novel human
 CC Note: This sequence data for this patent is not to appear in the printed
 CC specification, but was obtained in electronic format directly from WPI
 CC at ftp.wpi.int/pub/published_pat_sequences.

XX Sequence 3531 BP; 952 A; 901 C; 960 G; 718 T; 0 other;

Query Match 60.6%; Score 392.6; DB 23; Length 3531;

Best Local Similarity 99.0%; P: N: 3.1e-97;

Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 TCTATCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 106

DB 2951 TCTATCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3010

QY 107 TCAGAGGCAACCCCAATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 166

DB 3011 TCAGAGGCAACCCCAATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3070

QY 167 CCACGACGCT 226

DB 3071 CCACGACGCT 3130

QY 227 AGTATCGGAATGCT 286

DB 3131 AGTATCGGAATGCT 3190

QY 287 GAGTACGAGCT 346

DB 3191 GAGTACGAGCT 3250

QY 347 GCTCTGACGCT 406

DB 3251 GCTCTGACGCT 445

QY 407 KAGACGCT 3349

DB 3311 KAGACGCT 3310

XX

RESULT 13

AAS86762

ID AAS86762 standard; cDNA; 621 BP.

XX AAS86762;
 AC 13-FEB-2002 (first entry)
 DT 13-FEB-2002 (first entry)
 DE DNA encoding novel human diagnostic protein #21566.
 XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW Food supplement; medical imaging; diagnostic; genetic disorder; se.
 XX Homo sapiens.
 OS Homo sapiens.
 XX MO200175067-A2.
 PF 11-OCT-2001.
 XX 30-MAR-2001; 2001MO-US08631.
 PF 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX (HWE-) HWEQ INC.
 XX Drmanac RT, Liu C, Tang YT;
 FI WFI, 2001, 61932/73.
 DR P-FOLD, AG22575.
 XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT for genetic disorders or other traits and to assess
 PT biodiversity.
 XX Claim 1; SEQ ID No 22566; 103pp; English.
 XX The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC sequences are useful in identifying expressed genes. (I) is useful in gene therapy techniques
 CC for identifying expressed genes. (I) is useful to treat disease states involving
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (I) is useful for generating antibodies against it, detecting or
 CC identifying the presence of (II) in a sample, and as a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The invention also provides a method for identifying identification of mutations
 CC diagnostic for genetic disorders or other traits to assess biodiversity
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. Aspects of the invention represent novel human
 CC Not: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic form directly from WIPO
 CC at ftp.wipo.int/pub/published_Pct_sequences.
 XX Sequence 621 BP; 156 A; 155 C; 175 G; 135 T; 0 other;
 QQ
 Query Match 34.6%; Score 224.4; DB 23; Length 621;
 Best Local Similarity 57.8%; Pred. No. 1-51;
 Matches 225; Conservative 0; Mismatches 51; Indels 0; Gaps 0;
 QY 220 ATTACGATGATTCGGATATGCGCCACGAGGATGGAGGCCCTTTTACGGGCGCTCGAG 279
 DB 580 ATTACGATGATTCGGATATGCGCCACGAGGATGGAGGCCCTTTTACGGGCGCTCGAG 117
 QY 280 TGGATGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 339
 DB 118 TGGATGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 177
 QY 340 GACTTCGCTCTACACATGCAATGTCTCCGGGAGTTAGATTTGAGGCGCATCGGCC 399
 DB 178 GACTTCGCTCTACACATGCAATGTCTCCGGGAGTTAGATTTGAGGCGCATCGGCC 237
 QY 400 TTGTGGAAGACG 445
 DB 238 TTGTGGAAGACG 283
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 AC90603;
 ID AAC90603 standard; cDNA, 657 BP.
 XX AAC90603;
 AC AAC90603;
 ID 13-MAR-2001 (first entry)
 DE Rabbit sodium channel beta1 protein coding sequence.
 KW Rat; sodium channel beta1 protein, hirsuties, pain, sleep disorder;
 KW neurodegenerative disorder; mood disorder; muscle contraction; se.
 OS Oryctolagus cuniculus.
 XX MO200069912-A1.
 PF 23-NOV-2000.
 PR 12-MAY-2000; 2000MO-US013144.
 XX 14-MAY-1999; 99US-0134198.
 XX (WILL-) MILLENNIUM PHARM INC.
 XX Curtis RMJ;
 FI WFI, 2001-122743/13.
 DE New rat sodium channel beta-3 subunit gene isolated from a rat dorsal
 PF root ganglion cDNA library for use in chromosome mapping, forensic
 PT medicine, monitoring clinical trials and therapeutics.
 XX Disclosure; Pkg 5; 145pp; English.
 XX The present invention provides the protein and coding sequences of the
 CC beta-3 subunit of the sodium channel. The beta-3 subunit is involved in
 CC involved in the generation of pain and other sensory or perceptible nerve
 CC impulses. In the establishment and endurance of mood, neurodegenerative
 CC and sleep disorders, and in the control of muscle contraction, including
 CC movements such as the heartbeat, digestion and vascular tone. The
 CC beta-3 subunit is involved in the generation of pain and other sensory or
 CC assays, and in pharmacogenomics.
 XX Sequence 657 BP; 146 A; 181 C; 213 G; 117 T; 0 other;
 QQ
 Query Match 22.9%; Score 148.2; DB 22; Length 657;
 Best Local Similarity 57.7%; Pred. No. 1-46-30;
 Matches 333; Conservative 0; Mismatches 223; Indels 21; Gaps 3;
 QY 76 TGTGTGAGATGCTCTGACGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 135
 DB 61 TGTGTGAGATGCTCTGACGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
 QY 136 ATCTCTCTCTGATGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 195
 DB 131 ATCTCTCTCTGATGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 180
 QY 196 CG 246
 DB 181 CAGAGAGGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 240
 QY 247 GAGGTGAGAGGCCCTTTTACGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 297
 DB 241 GAGGTGAGAGGCCCTTTTACGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300

Faraday Avenue Genoscope sequence ID : CS0DF023A05QPT.

FEATURES

```

SOURCE
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   /db_xref="taxon:9606"
   /clone="CS0DF023A09"
   /clone_lib="FETAL BRAIN"
   /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo (GT) primer. Five prime end
cloned double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."
BASE COUNT      291 a   289 c   334 g   243 t   44 others
ORIGIN
Query Match      99.7%; Score 646; DB 13; Length 1201;
Best Local Similarity 99.7%; Pred. No. 5.5e-163;
Matches 646; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGCTGCTGCTTCAATAGATTGTTCCCTGCTCTCTGCTGCTATCTATCTGCTCACT 60
Db 2 ATGCTGCTGCTTCAATAGATTGTTCCCTGCTCTCTGCTGCTATCTATCTGCTCACT 351
Qy 61 GTCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
Db 352 GTCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 411
Qy 121 ATGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
Db 412 ATGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 471
Qy 181 GAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
Db 472 GAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 531
Qy 241 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
Db 532 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 591
Qy 301 GAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
Db 592 GAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 651
Qy 361 ATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Db 652 ATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 711
Qy 421 ATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
Db 712 ATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 771
Qy 481 ATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
Db 772 ATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 831
Qy 541 TAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
Db 832 TAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 891
Qy 601 ATCTCATCTGAGACACAGAGACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 648
Db 892 ATCTCATCTGAGACACAGAGACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 939

RESULT 2
LOCUS      5602
DEFINITION Homo sapiens FETAL BRAIN Homo sapiens cDNA Clone
            CS0DF023A09 5-PRIME, mRNA sequence.
ACCESSION  BX45002

```

Version 2.2.1

Source 1

Organism

Reference

Authors

Title

Comment

Genoscope - Centre National de Sequencage

BP 191 91006 Evry cedex - France

Email: seqref@genoscope.cns.fr; Web : www.genoscope.cns.fr

Invitrogen. This sequence belongs to sequence cluster 6147.r For

more information about this cluster, see

http://www.genoscope.cns.fr/

http://www.genoscope.cns.fr/

http://fulllength.invitrogen.com/Invitrogen Corporation 1600

Paradise Avenue Genoscope sequence ID : CS1AF0062B09Q1.

Location/Qualifiers

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS1AF0062B09Q1"

/clone_lib="FETAL BRAIN"

/dev_stage="fetal"

/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA

was primed with a NotI-oligo (GT) primer. Five prime end

cloned double-strand cDNA was digested with Not I and

cloned into the Not I and EcoRV sites of the pCMVSPORT 6

vector. Library was not normalized."

BASE COUNT 273 a 292 c 336 g 247 t 53 others

ORIGIN

Query Match 96.4%; Score 624.4; DB 13; Length 1201;

Best Local Similarity 96.4%; Pred. No. 1.5e-157;

Matches 636; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

Qy 1 ATGCTGCTGCTTCAATAGATTGTTCCCTGCTCTCTGCTGCTATCTATCTGCTCACT 60

Db 282 ATGCTGCTGCTTCAATAGATTGTTCCCTGCTCTCTGCTGCTATCTATCTGCTCACT 341

Qy 61 GTCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120

Db 342 GTCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 401

Qy 121 ATGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180

Db 402 ATGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 461

Qy 181 GAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240

Db 462 GAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 521

Qy 241 CACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300

Db 522 CACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 581

Qy 301 GAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360

Db 582 GAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 641

Qy 361 ATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420

Db 642 ATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 701

Qy 421 ATCTCCCTTCAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480

	Matches	109;	Conservative	0;	Mismatches	121;	Indels	0;	Gaps	0;
Qy	243	CHAGAGGTGTGAGAGCCCTTTTCAGGGGCGCTCTGTCAGTGTGATGAGCAGCAGAGACTGTGA	302							
Qy	1050	CTGCT	1109							
Qy	303	GGAGTGTGCTATCATCTCTGCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	362							
Db	1110	GGAGGCGCCCTCTGCGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1159							
Qy	363	TGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	422							
Qy	1170	CGCGCGCT	1229							
Qy	423	CGCGCT	472							
Db	1210	CGCGCT	1279							

Db 8318 GGAGCGCCCGCCGCGCGAGCTGAAGCTGCCGGGATGCCGAGCGCTTCGACACGAGT 8377
 Qy 363 TGTGTCGGGAGGTTTGATTTGAGCGGATGAGCGCTCTTTTGTGAAGAGCGGGCTGAT 422
 Db 8378 CCGCGCGCGCGAGAGCCGCGCTCAAGAGGATACCGCGCGCGAGCGCTGCGCCCGGCT 8437
 Qy 423 CCGCTTAAGAGTTCGCGAGCGGAGCGCTTGTGAGAGATTTTGTACCTCTTGATGCTT 472
 Db 8438 CCGCGCGGCTCGCATCGAGCGGAGCTGCTGATCTTCGCTCGGCGACT 8487

RESULT 4
 US-09-726-614-13
 ; Sequence 13, Application US/09726614
 ; Patent No. 6514735
 ; INVENTOR: S. Jensen
 ; APPLICANT: Susan E. Jensen
 ; APPLICANT: Kwame A. Aidoo
 ; APPLICANT: Ashish S. Paradkar
 ; TITLE OF INVENTION: DNA Sequence Encoding Enzymes of Clavulanic
 ; Patent No. 6514735
 ; TITLE OF INVENTION: Acid Biosynthesis
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS: PRICE, HOLMAN & STERN PLLC
 ; ADDRESS: JACOBSON, PRICE, HOLMAN & STERN PLLC
 ; STREET: The Joffier Building, 400 Seventh Street, N.W.
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: U.S.A.
 ; ZIP: 20005
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; SOFTWARE: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/726-614
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/790,462
 ; FILING DATE: 29-JAN-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: D. Douglas Price
 ; REGISTRATION NUMBER: 24,514
 ; REFERENCE/DOCKET NUMBER: 1418/P57452US2
 ; TELEPHONE: (202) 638-6666
 ; TELEPHONE: (202) 39305350
 ; TELEFAX: (202) 39305350
 ; INFO: RCN 248593 IDEA UR
 ; INFO: RCN 248593 IDEA UR
 ; SEQUENCE CHARACTERISTICS:
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; HYPOTHETICAL: NO
 ; ORIGINAL SOURCE:
 ; ORGANISM: Streptomyces clavuligerus
 ; US-09-726-614-13

Query Match 5.68; Score 36.4; DB 4; Length 11604;
 Best Local Similarity 47.44; Pred. No. 3;
 Matches 109; Conservative 0; Mismatches 121; Indels 0; Gaps 0;
 Qy 243 CCAAGAGCGGAGAGCCCTTTTCAAGGCGCGCTCTGATGATGAGAGGAGACTTCA 302
 Db 8258 CTTGAGCGCTAGAGCATTTGAGCATTCGATCCGATCGGCGCCGAGGCGACCT 8317
 Qy 303 GAGAGTGTGATCATCTGTCTCAAGCTCATCTGAAGCATCTGCGCTCTCAACTGCA 362
 Db 8318 GGAGCGCGCGCGCGAGCTGATGCTGCGAGTTCGAGTTCGCGACTTCGCGACT 8377
 Qy 363 TGTGTCGGGAGGTTTGATTTGAGCGGATGAGCGCTCTTTTGTGAAGAGCGGGCTGAT 422

Db 8378 CCGCGCGCGCGAGAGCCGCGCTCAAGAGGATACCGCGCGAGCGCTGCGCCCGGCT 8437
 Qy 423 CCGCTTAAGAGTTCGCGAGCGGAGCGCTTGTGAGAGATTTTGTACCTCTTGATGCTT 472
 Db 8438 CCGCGCGGCTCGCATCGAGCGGAGCTGCTGATCTTCGCTCGGCGACT 8487

RESULT 5
 US-09-385-028-1
 ; Sequence 1, Application US/09385028
 ; Patent No. 6232106
 ; GENERAL INFORMATION:
 ; INVENTOR: S. Jensen
 ; APPLICANT: Susan E. Jensen
 ; APPLICANT: Kwame A. Aidoo
 ; APPLICANT: Ashish S. Paradkar
 ; TITLE OF INVENTION: DNA Sequence Encoding Enzymes of Clavulanic
 ; Patent No. 6232106
 ; TITLE OF INVENTION: Acid Biosynthesis
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS: PRICE, HOLMAN & STERN PLLC
 ; ADDRESS: JACOBSON, PRICE, HOLMAN & STERN PLLC
 ; STREET: The Joffier Building, 400 Seventh Street, N.W.
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: U.S.A.
 ; ZIP: 20005
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; SOFTWARE: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/385-028
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/790,462
 ; FILING DATE: 29-JAN-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: D. Douglas Price
 ; REGISTRATION NUMBER: 24,514
 ; REFERENCE/DOCKET NUMBER: 1418/P57452US2
 ; TELEPHONE: (202) 638-6666
 ; TELEPHONE: (202) 39305350
 ; INFO: RCN 248593 IDEA UR
 ; INFO: RCN 248593 IDEA UR
 ; SEQUENCE CHARACTERISTICS:
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; HYPOTHETICAL: NO
 ; ORIGINAL SOURCE:
 ; ORGANISM: Streptomyces clavuligerus
 ; US-09-385-028-1

Query Match 5.68; Score 36.4; DB 3; Length 15079;
 Best Local Similarity 47.44; Pred. No. 3;
 Matches 109; Conservative 0; Mismatches 121; Indels 0; Gaps 0;
 Qy 243 CCAAGAGCGGAGAGCCCTTTTCAAGGCGCGCTCTGATGATGAGAGGAGACTTCA 302
 Db 10290 CTTGAGCGCTAGAGCATTTGAGCATTCGATCCGATCGGCGCCGAGGCGACCT 10349
 Qy 303 GAGAGTGTGATCATCTGTCTCAAGCTCATCTGAAGCATCTGCGCTCTCAACTGCA 362
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 Qy 363 TGTGTCGGGAGGTTTGATTTGAGCGGATGAGCGCTCTTTTGTGAAGAGCGGGCTGAT 422
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QY 423 CCCCCCTAAGAGTCCAGGAGGCTGAGAGGACTTCAACCTCTGTGTCT 472
 DB 10470 CCCCCCTGAGGCTGAGAGGCTGAGAGGCTTCAACCTCTGTGTCT 10519

RESULTS

Sequence 1, Application US/09726614
 GENERAL INFORMATION:
 APPLICANT: E. Jensen
 APPLICANT: Kwamena A. Aidoo
 APPLICANT: Ashish S. Paradar
 TITLE OF INVENTION: DNA Sequence Encoding Enzymes of Clavulanic
 PATENT NO. 6514735
 TITLE OF INVENTION: Acid Biosynthesis
 NUMBER OF SEQUENCES: 25
 CORRESPONDENCE ADDRESS: PRICE, WOMAN & STEIN, P.L.C.
 STREET: The Jennifer Building, 400 Seventh Street, N.W.
 CITY: Washington
 STATE: D.C.
 ZIP: 20004
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30 (RFO)
 CURRENT APPLICATION DATA:
 FILING DATE: US/09/726,614
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/790,462
 ATTORNEY/AGENT INFORMATION:
 NAME: D. Douglas Price
 REGISTRATION NUMBER: 24,514
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 638-6666
 TELEFAX: (202) 638-6666
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15079 base pairs
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 ORIGINAL SOURCE:
 ORGANISM: Streptomyces clavuligerus
 US-09-726-614-1

Query Match 5.6%; Score 36.4; DB 4; Length 15079;
 Best Local Similarity 47.4%; Pred. No. 3;
 Matches 109; Conservative 0; Mismatches 121; Indels 0; Gaps 0;
 QY 243 CCAGAGAGTGAGAGCCCTTTTCAGGGGCGCTGAGTGAGTGGAGGAGGAGCTGCA 302
 DB 10290 CTTGAGCGCTTCAAGAGCTTTCACCGCTTCCCTGCGCCGAGGAGCCGCGGCTCA 10349
 QY 303 GAGCTGATCATCTGTGCTTCAAGCTCTGACTCTGAAGCTCTTGCTCTTACATCTCA 362
 DB 10350 GAGAGCGCCGCGCGGCGAGCTGAGCTGCGCGAGATGCCCGAGCTTCCGACACAGAT 10409
 QY 363 TGTCTTCGCGAGGTTTGAGTTTGAGCGCATCGGCCCTTTCTTGAGAGAGACCGCGAT 422
 DB 10410 CCGCCGCCGAGAGACCGCGCTCAAGGATACCGCGCCGCGCGCGCTCCCGCGGCT 10469

QY 423 CCCCCCTAAGAGTCCAGGAGGCTGAGAGGACTTCAACCTCTGTGTCT 472
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RESULT 7

US/09-243-308
 Sequence 388, Application US/0996243
 Patent No. 6478825
 GENERAL INFORMATION:
 APPLICANT: Ashish S. Paradar
 APPLICANT: Bates, Kevin P.
 APPLICANT: Berstein, David
 APPLICANT: Deenoyers, Luc
 APPLICANT: Deenoyers, Patricia Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gertler, Mary B.
 APPLICANT: Gertler, Paul J.
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Gurney, David A.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Peoni, Nicholas F.
 APPLICANT: Peoni, Nicholas F.
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tamas, Daniel
 APPLICANT: Tamas, Colin K.
 APPLICANT: Tamas, Michael
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ACID SEQUENCES ENCODING THE SAME
 FILING DATE: 2001-11-14
 CURRENT APPLICATION NUMBER: US/09/996,243
 PRIOR APPLICATION NUMBER: 60/043787
 PRIOR FILING DATE: 2001-11-14
 PRIOR APPLICATION NUMBER: 60/062250
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/065186
 PRIOR FILING DATE: 1997-11-13
 PRIOR APPLICATION NUMBER: 60/065311
 PRIOR FILING DATE: 1997-11-13
 PRIOR APPLICATION NUMBER: 60/066770
 PRIOR FILING DATE: 1998-02-25
 PRIOR APPLICATION NUMBER: 60/078910
 PRIOR FILING DATE: 1998-04-28
 PRIOR APPLICATION NUMBER: 60/081322
 PRIOR FILING DATE: 1998-04-28
 PRIOR APPLICATION NUMBER: 60/084600
 PRIOR FILING DATE: 1998-05-28
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 PRIOR APPLICATION NUMBER: 60/088026
 PRIOR FILING DATE: 1998-06-04

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 6 PRIOR APPLICATION NUMBER: 60/088030
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 9 PRIOR FILING DATE: 1998-06-04
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 12 PRIOR APPLICATION NUMBER: 60/088167
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 31 PRIOR FILING DATE: 1998-06-10
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 33 PRIOR FILING DATE: 1998-06-10
 34 PRIOR APPLICATION NUMBER: 60/088858
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 42 PRIOR APPLICATION NUMBER: 60/089440
 43 PRIOR FILING DATE: 1998-06-16
 44 PRIOR APPLICATION NUMBER: 60/089512
 45 PRIOR FILING DATE: 1998-06-16
 46 PRIOR APPLICATION NUMBER: 60/089514
 47 PRIOR FILING DATE: 1998-06-16
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 49 PRIOR FILING DATE: 1998-06-17
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 51 PRIOR FILING DATE: 1998-06-17
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 56 PRIOR APPLICATION NUMBER: 60/089600
 57 PRIOR FILING DATE: 1998-06-17
 58 PRIOR APPLICATION NUMBER: 60/089653
 59 PRIOR FILING DATE: 1998-06-17
 60 PRIOR APPLICATION NUMBER: 60/089801
 61 PRIOR FILING DATE: 1998-06-18
 62 PRIOR APPLICATION NUMBER: 60/089907
 63 PRIOR FILING DATE: 1998-06-18
 64 PRIOR APPLICATION NUMBER: 60/089947
 65 PRIOR FILING DATE: 1998-06-19
 66 PRIOR APPLICATION NUMBER: 60/089948
 67 PRIOR FILING DATE: 1998-06-19
 68 PRIOR APPLICATION NUMBER: 60/089952
 69 PRIOR FILING DATE: 1998-06-19
 70 PRIOR APPLICATION NUMBER: 60/090246
 71 PRIOR FILING DATE: 1998-06-22
 72 PRIOR APPLICATION NUMBER: 60/090252

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 2 PRIOR APPLICATION NUMBER: 60/090254
 3 PRIOR FILING DATE: 1998-06-22
 4 PRIOR APPLICATION NUMBER: 60/090349
 5 PRIOR FILING DATE: 1998-06-22
 6 PRIOR APPLICATION NUMBER: 60/090355
 7 PRIOR FILING DATE: 1998-06-23
 8 PRIOR APPLICATION NUMBER: 60/090429
 9 PRIOR FILING DATE: 1998-06-24
 10 PRIOR APPLICATION NUMBER: 60/090431
 11 PRIOR FILING DATE: 1998-06-24
 12 PRIOR APPLICATION NUMBER: 60/090435
 13 PRIOR FILING DATE: 1998-06-24
 14 PRIOR APPLICATION NUMBER: 60/090444
 15 PRIOR FILING DATE: 1998-06-24
 16 PRIOR APPLICATION NUMBER: 60/090445
 17 PRIOR FILING DATE: 1998-06-24
 18 PRIOR APPLICATION NUMBER: 60/090472
 19 PRIOR FILING DATE: 1998-06-24
 20 PRIOR APPLICATION NUMBER: 60/090535
 21 PRIOR FILING DATE: 1998-06-24
 22 PRIOR APPLICATION NUMBER: 60/090540
 23 PRIOR FILING DATE: 1998-06-24
 24 PRIOR APPLICATION NUMBER: 60/090542
 25 PRIOR FILING DATE: 1998-06-24
 26 PRIOR APPLICATION NUMBER: 60/090557
 27 PRIOR FILING DATE: 1998-06-25
 28 PRIOR APPLICATION NUMBER: 60/090676
 29 PRIOR FILING DATE: 1998-06-25
 30 PRIOR APPLICATION NUMBER: 60/090678
 31 PRIOR FILING DATE: 1998-06-25
 32 PRIOR APPLICATION NUMBER: 60/090690
 33 PRIOR FILING DATE: 1998-06-25
 34 PRIOR APPLICATION NUMBER: 60/090694
 35 PRIOR FILING DATE: 1998-06-25
 36 PRIOR APPLICATION NUMBER: 60/090695
 37 PRIOR FILING DATE: 1998-06-25
 38 PRIOR APPLICATION NUMBER: 60/090696
 39 PRIOR FILING DATE: 1998-06-26
 40 PRIOR APPLICATION NUMBER: 60/090862
 41 PRIOR FILING DATE: 1998-06-26
 42 PRIOR APPLICATION NUMBER: 60/090863
 43 PRIOR FILING DATE: 1998-06-26
 44 PRIOR APPLICATION NUMBER: 60/091160
 45 PRIOR FILING DATE: 1998-07-01
 46 PRIOR APPLICATION NUMBER: 60/091478
 47 PRIOR FILING DATE: 1998-07-02
 48 PRIOR APPLICATION NUMBER: 60/091544
 49 PRIOR FILING DATE: 1998-07-02
 50 PRIOR APPLICATION NUMBER: 60/091519
 51 PRIOR FILING DATE: 1998-07-02
 52 PRIOR APPLICATION NUMBER: 60/091626
 53 PRIOR FILING DATE: 1998-07-02
 54 PRIOR APPLICATION NUMBER: 60/091633
 55 PRIOR FILING DATE: 1998-07-02
 56 PRIOR APPLICATION NUMBER: 60/091978
 57 PRIOR FILING DATE: 1998-07-07
 58 PRIOR APPLICATION NUMBER: 60/091982
 59 PRIOR FILING DATE: 1998-07-07
 60 PRIOR APPLICATION NUMBER: 60/092182
 61 PRIOR FILING DATE: 1998-07-07
 62 PRIOR APPLICATION NUMBER: 60/092183
 63 PRIOR FILING DATE: 1998-07-07

Query Match: 5.6%; Score 36.2; DB 4; Length 1371;

Best Local Similarity 49.2%; Pred. No. 1.4; Matches 93; Conservative 0; Mismatch 98; Indels 0; Gaps 0;

QY 198 CGAGGCGGCTAAGATTCCTTTATTCAGGTATCGATATGCCACGAGCGTGGAG 257
 Db 327 CGGCGCACTTCAGGCGCTGCTTTATTCACACACATAGTCTCTTCAACCCCTG 386
 QY 258 CCGCTTTAGAGCGCGCTCGATCGATCGATCGACGACGCTCGACGACGTCTC 317
 Db 387 CGCGTTTAGAGACCGGCTCTCTTGGAGTGGAGATCCTTGGCGGACGATCCCT 446

Db 1011 TGTGATCTCCACCTCTCGCGGCGACGCGTTTCGACTCATGCTGGCGGCGCATCTTCCGCC 972
 Qy 245 AGAGCTGTGAGAGCCCTTTTCAGGCGGCTCGTCAGTGAATGCGACAGAGACTCGGAG 304
 Db 971 ACGAGGTCCTCCGACCGCGCGCGCTGCTGCTTCATCATCTGCGACATCTGAGG 912
 Qy 305 ACCTCTCATCACTGCTCTCAAGTCACTCTGAAGCACTCTGCGCTCTACACTCGCAATG 364
 Db 911 AGCTGTGCTGCGAGCTTTTCGCGCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 852
 Qy 365 TGCTTCGCGGAGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 395
 Db 915 TGTTCGCGGAGACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 821

RESULT 11

US-09-423-439-25
 Patent No. 6339070
 GENERAL INFORMATION:
 APPLICANT: EMERY, Stephen Charles
 TITLE OF INVENTION: CHEMICAL COMPOUNDS
 NUMBER OF SEQUENCES: 60
 CORRESPONDENCE ADDRESS:
 ADDRESS: 1100 New York Ave., L.L.P.
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER SYSTEM: IBM compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: MS Word
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/423,439
 FILING DATE: 09-NOV-1997
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/GB98/01294
 FILING DATE: 10-MAY-1997
 APPLICATION NUMBER: GB 9709421.3
 FILING DATE: 10-MAY-1997
 INFORMATION FOR SEQ ID NO: 25:
 SEQUENCE LENGTH: 1926 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 MOLECULE TYPE: other nucleic acid
 SEQUENCE DESCRIPTION: SEQ ID NO: 25:

US-09-423-439-25
 Query Match 5.5%; Score 35.8; DB 4; Length 1926;
 Best Local Similarity 52.3%; Pred. No. 2;
 Matches 79; Conservative 0; Mismatches 72; Indels 0; Gaps 0;
 Qy 270 GCGCTCGCATGTGATGATGCGAGGACTCTGCGAGCTGTCATCTGTCGTCACGCT 329
 Db 1464 GCGCTTCGATGACCATCTCGAAGCGCGCGGCGGACCTCGAATCATATCTCCCGCACGCGC 1523
 Qy 330 CAGCTTCGATGACCATCTCGAAGCGCGCGGCGGACCTCGAATCATATCTCCCGCACGCGC 389
 Db 1524 CAGCTTCGATGACCATCTCGAAGCGCGCGGCGGACCTCGAATCATATCTCCCGCACGCGC 1583
 Qy 390 GATGCGGCTCTTTTGAGACGACGCGGCTG 420
 Db 1584 GCTGAGAGAGCGCGCGGCGGACGAGAGAGCTG 1614
 US-09-423-439-25
 Query Match 5.5%; Score 35.8; DB 4; Length 1926;
 Best Local Similarity 52.3%; Pred. No. 2;
 Matches 79; Conservative 0; Mismatches 72; Indels 0; Gaps 0;
 Qy 270 GCGCTCGCATGTGATGATGCGAGGACTCTGCGAGCTGTCATCTGTCGTCACGCT 329
 Db 1464 GCGCTTCGATGACCATCTCGAAGCGCGCGGCGGACCTCGAATCATATCTCCCGCACGCGC 1523
 Qy 330 CAGCTTCGATGACCATCTCGAAGCGCGCGGCGGACCTCGAATCATATCTCCCGCACGCGC 389
 Db 1524 CAGCTTCGATGACCATCTCGAAGCGCGCGGCGGACCTCGAATCATATCTCCCGCACGCGC 1583
 Qy 390 GATGCGGCTCTTTTGAGACGACGCGGCTG 420
 Db 1584 GCTGAGAGAGCGCGCGGCGGACGAGAGAGCTG 1614

RESULT 12

US-09-423-439-15
 Sequence 15, Application US/09423439
 Patent No. 6339070
 GENERAL INFORMATION:
 APPLICANT: EMERY, Stephen Charles
 TITLE OF INVENTION: CHEMICAL COMPOUNDS
 NUMBER OF SEQUENCES: 60
 CORRESPONDENCE ADDRESS:
 ADDRESS: 1100 New York Ave., L.L.P.
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER SYSTEM: IBM compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: MS Word
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/423,439
 FILING DATE: 09-NOV-1997
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/GB98/01294
 FILING DATE: 10-MAY-1997
 APPLICATION NUMBER: GB 9709421.3
 FILING DATE: 10-MAY-1997
 INFORMATION FOR SEQ ID NO: 15:
 SEQUENCE LENGTH: 1929 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 MOLECULE TYPE: other nucleic acid
 SEQUENCE DESCRIPTION: SEQ ID NO: 15:

US-09-423-439-15
 Query Match 5.5%; Score 35.8; DB 4; Length 1929;
 Best Local Similarity 52.3%; Pred. No. 2;
 Matches 79; Conservative 0; Mismatches 72; Indels 0; Gaps 0;
 Qy 270 GCGCTCGCATGTGATGATGCGAGGACTCTGCGAGCTGTCATCTGTCGTCACGCT 329
 Db 1467 GCGCTTCGATGACCATCTCGAAGCGCGCGGCGGACCTCGAATCATATCTCCCGCACGCGC 1526
 Qy 330 CAGCTTCGATGACCATCTCGAAGCGCGCGGCGGACCTCGAATCATATCTCCCGCACGCGC 389
 Db 1527 CAGCTTCGATGACCATCTCGAAGCGCGCGGCGGACCTCGAATCATATCTCCCGCACGCGC 1586
 Qy 390 GATGCGGCTCTTTTGAGACGACGCGGCTG 420
 Db 1587 GCTGAGAGAGCGCGCGGCGGACGAGAGAGCTG 1617
 US-09-423-439-15
 Query Match 5.5%; Score 35.8; DB 4; Length 1929;
 Best Local Similarity 52.3%; Pred. No. 2;
 Matches 79; Conservative 0; Mismatches 72; Indels 0; Gaps 0;
 Qy 270 GCGCTCGCATGTGATGATGCGAGGACTCTGCGAGCTGTCATCTGTCGTCACGCT 329
 Db 1467 GCGCTTCGATGACCATCTCGAAGCGCGCGGCGGACCTCGAATCATATCTCCCGCACGCGC 1526
 Qy 330 CAGCTTCGATGACCATCTCGAAGCGCGCGGCGGACCTCGAATCATATCTCCCGCACGCGC 389
 Db 1527 CAGCTTCGATGACCATCTCGAAGCGCGCGGCGGACCTCGAATCATATCTCCCGCACGCGC 1586
 Qy 390 GATGCGGCTCTTTTGAGACGACGCGGCTG 420
 Db 1587 GCTGAGAGAGCGCGCGGCGGACGAGAGAGCTG 1617

RESULT 13

US-09-252-991A-3322
 Sequence 3322, Application US/09252991A
 Patent No. 6339070
 GENERAL INFORMATION:
 APPLICANT: Marc J. Rubinfeld et al.
 TITLE OF INVENTION: PEPTIDES FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: 07/171,911
 CURRENT APPLICATION NUMBER: US/09/252,991A
 CURRENT FILING DATE: 1999-02-18
 PRIOR APPLICATION NUMBER: US 60/074,788
 PRIOR FILING DATE: 1998-07-27
 PRIOR APPLICATION NUMBER: US 60/094,190
 NUMBER OF SEQ ID NOS: 33142
 SEQ ID NO 3322

RESULT 14

US-09-252-991A-3322
 Sequence 3322, Application US/09252991A
 Patent No. 6339070
 GENERAL INFORMATION:
 APPLICANT: Marc J. Rubinfeld et al.
 TITLE OF INVENTION: PEPTIDES FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: 07/171,911
 CURRENT APPLICATION NUMBER: US/09/252,991A
 CURRENT FILING DATE: 1999-02-18
 PRIOR APPLICATION NUMBER: US 60/074,788
 PRIOR FILING DATE: 1998-07-27
 PRIOR APPLICATION NUMBER: US 60/094,190
 NUMBER OF SEQ ID NOS: 33142
 SEQ ID NO 3322

Mon Dec 8 11:25:49 2003

us-09-936-680-4_copy_376_1023.rn1

Page 9

[illegible]

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RESULT 2
US-09-997-579-3
SEQUENCE 3, APPLICATION US/0999579
GENERAL INFORMATION
APPLICANT: Cambridge University Technical Services
TITLE OF INVENTION: A novel family of beta sub-unit proteins from a voltage gated sod
FILE OF INVENTION: chenna
FILE REFERENCE: 674558-2011
CURRENT APPLICATION NUMBER: US/09/997,579
CURRENT FILING DATE: 2009-04-05
PRIORITY CLAIMED FROM: EP000031793
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 60,129,473
PRIOR FILING DATE: 2000-02-24
INVENTOR: Srinivasan, Ravi
SOFTWARE: patentin version 3.1
SEQ ID NO 3
LENGTH: 2220
TYPE: CDS
ORGANISM: rat
US-09-997-579-3

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181	GAATGTTCTTCAAGGAGCCCGAGGCGGTAAAGATTTCTTATTAACAGTATTCGGAATGCG	241	
182	GAATGTTCTTCAAGGAGCCCGAGGCGGTAAAGATTTCTTATTAACAGTATTCGGAATGCG	242	
642	GACGAGGTTTTCAGAGGCTTCAAGGCGGTAAAGATTTCTTATTAACAGTATTCGGAATGCG	603	
241	CACGAGGTTTTCAGAGGCTTCAAGGCGGTAAAGATTTCTTATTAACAGTATTCGGAATGCG	300	
242	CACGAGGTTTTCAGAGGCTTCAAGGCGGTAAAGATTTCTTATTAACAGTATTCGGAATGCG	301	
603	CACGAGGTTTTCAGAGGCTTCAAGGCGGTAAAGATTTCTTATTAACAGTATTCGGAATGCG	662	
604	CACGAGGTTTTCAGAGGCTTCAAGGCGGTAAAGATTTCTTATTAACAGTATTCGGAATGCG	663	
301	CAGAGACGTGTCATCTGCTGCTCAAGCTCACTCTGACAGCATCTGCGCTCTCAACCTGC	360	
302	CAGAGACGTGTCATCTGCTGCTCAAGCTCACTCTGACAGCATCTGCGCTCTCAACCTGC	361	
663	CAGAGACGTGTCATCTGCTGCTCAAGCTCACTCTGACAGCATCTGCGCTCTCAACCTGC	722	
664	CAGAGACGTGTCATCTGCTGCTCAAGCTCACTCTGACAGCATCTGCGCTCTCAACCTGC	723	
361	AATGATGTCCTCGGAGGCTTGAAGTTGAGTTCGAGCGGAGATCGGCTTTTGAGACGACGCGCTG	420	
362	AATGATGTCCTCGGAGGCTTGAAGTTGAGTTCGAGCGGAGATCGGCTTTTGAGACGACGCGCTG	421	
723	AATGATGTCCTCGGAGGCTTGAAGTTGAGTTCGAGCGGAGATCGGCTTTTGAGACGACGCGCTG	782	
724	AATGATGTCCTCGGAGGCTTGAAGTTGAGTTCGAGCGGAGATCGGCTTTTGAGACGACGCGCTG	783	
421	ATTCGCCCTTAAGGTGTCACGAGGAGCGCGAGAGAGCTCACTCTGTGCTTCAAGAAATC	480	
422	ATTCGCCCTTAAGGTGTCACGAGGAGCGCGAGAGAGCTCACTCTGTGCTTCAAGAAATC	481	
783	ATGATGCTTACGCGCTTCAAGGAGGAGCGAGAGAGCTCACTCTGTGCTTCAAGAAATC	842	
784	ATGATGCTTACGCGCTTCAAGGAGGAGCGAGAGAGCTCACTCTGTGCTTCAAGAAATC	843	
481	ATGATGCTTACGCGCTTCAAGGAGGAGCGAGAGAGCTCACTCTGTGCTTCAAGAAATC	540	
482	ATGATGCTTACGCGCTTCAAGGAGGAGCGAGAGAGCTCACTCTGTGCTTCAAGAAATC	541	
843	ATGATGCTTACGCGCTTCAAGGAGGAGCGAGAGAGCTCACTCTGTGCTTCAAGAAATC	902	
844	ATGATGCTTACGCGCTTCAAGGAGGAGCGAGAGAGCTCACTCTGTGCTTCAAGAAATC	903	
541	TACGAGAAAGGCTCTTAAGGCGCGAGAGGCGGCGAGAGAGAGAGGCGTCTGACTACTCTCC	600	
542	TACGAGAAAGGCTCTTAAGGCGCGAGAGGCGGCGAGAGAGAGAGGCGTCTGACTACTCTCC	601	
903	TACGAGAAAGGCTCTTAAGGCGCGAGAGGCGGCGAGAGAGAGAGGCGTCTGACTACTCTCC	962	
904	TACGAGAAAGGCTCTTAAGGCGCGAGAGGCGGCGAGAGAGAGAGGCGTCTGACTACTCTCC	963	
601	ATTCCTCTTACGAGAAACGAGAGAACTCTGTGTGTACTCTGTGAGGAGATA	647	
602	ATTCCTCTTACGAGAAACGAGAGAACTCTGTGTGTACTCTGTGAGGAGATA	648	
963	ATTCCTCTTACGAGAAACGAGAGAACTCTGTGTGTACTCTGTGAGGAGATA	1009	

[illegible]

Db 181 GAGTGGTCTACAGGCTGAGGCGGTAAAGATTCTTATATAGTATCGAATGCG 240
 Qy 241 CACCAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 300
 Db 241 CACCAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 300
 Qy 301 CAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360
 Db 301 CAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360
 Qy 361 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
 Db 361 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
 Qy 421 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 480
 Db 421 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 480
 Qy 481 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 540
 Db 481 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 540
 Qy 541 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 600
 Db 541 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 600
 Qy 601 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 645
 Db 601 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 645

RESULT 6

US-10-029-131-23
 ; Sequence 23, Application US/10029191
 ; Publication No. US20020160453A1
 ; INVENTOR: Kory A.J.
 ; APPLICANT: CURTIS
 ; TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT
 ; TITLE OF INVENTION: PROTEIN
 ; CURRENT FILING DATE: 2001-12-20
 ; PRIOR APPLICATION NUMBER: US/10/029,191
 ; PRIOR FILING DATE: 2001-12-20
 ; PRIOR APPLICATION NUMBER: 09/569,978
 ; PRIOR FILING DATE: 1999-05-14
 ; NUMBER OF SEQ ID NOS: 23
 ; SEQ ID NO 23 Patent In Ver. 2.1
 ; LENGTH: 657
 ; TYPE: DNA
 ; TYPE: DNA
 ; US-10-029-131-23

Query Match 22.9%; Score 148.21; DB 13; Length 657;
 Best Local Similarity 56.7%; Pred. No. 7,9e-34;
 Matches 333; Conservative
 Qy 76 TGTGTGAGAGTGGCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 135
 Db 61 TGTGTGAGAGTGGCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
 Qy 136 ATTCTTCTACAG 195
 Db 121 ATTCTTCTACAG 180
 Qy 196 CCGAG 246
 Db 181 CAG 240
 Qy 247 GAGGTGAG 297
 Db 241 GAG 300

Qy 298 CTGAG 357
 Db 301 CTGAG 360
 Qy 358 TGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
 Db 358 TGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
 Qy 417 TGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 477
 Db 417 TGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 477
 Qy 418 CTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 480
 Db 421 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 490
 Qy 478 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 537
 Db 481 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 540
 Qy 538 TGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 594
 Db 541 TGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 600
 Qy 595 CTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 631
 Db 601 TGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 637

RESULT 7

US-09-917-800A-1654
 ; Sequence 1654, Application US/09917800A
 ; Patent No. US20020119462A1
 ; INVENTOR: Robert Johnson, Donna
 ; APPLICANT: Johnson, Kory
 ; APPLICANT: Castile, Arthur
 ; APPLICANT: Castile, Arthur
 ; APPLICANT: Gene Logic, Inc.
 ; TITLE OF INVENTION: Molecular Toxicology Modeling
 ; FILE REFERENCE: 44921-5038-US /09/917,800A
 ; CURRENT FILING DATE: 2001-07-31
 ; PRIOR APPLICATION NUMBER: US 60/222,040
 ; PRIOR FILING DATE: 2000-07-31
 ; PRIOR APPLICATION NUMBER: 00/222,040
 ; PRIOR FILING DATE: 2000-11-02
 ; PRIOR APPLICATION NUMBER: US 60/290,029
 ; PRIOR FILING DATE: 2001-05-15
 ; PRIOR APPLICATION NUMBER: 00/290,045
 ; PRIOR FILING DATE: 2001-05-15
 ; PRIOR APPLICATION NUMBER: US 60/292,336
 ; PRIOR FILING DATE: 2001-05-22
 ; PRIOR APPLICATION NUMBER: 00/295,798
 ; PRIOR FILING DATE: 2001-06-06
 ; PRIOR APPLICATION NUMBER: US 60/297,457
 ; PRIOR FILING DATE: 2001-06-13
 ; PRIOR APPLICATION NUMBER: 00/298,884
 ; PRIOR FILING DATE: 2001-06-19
 ; PRIOR APPLICATION NUMBER: US 60/303,459
 ; PRIOR FILING DATE: 2001-07-09
 ; NUMBER OF SEQ ID NOS: 2
 ; SEQ ID NO 1654
 ; LENGTH: 1490
 ; TYPE: DNA
 ; TYPE: DNA
 ; ORGANISM: Rattus norvegicus
 ; OTHER INFORMATION: Genbank Accession No. US20020119462A1 NW_017288
 ; US-09-917-800A-1654

Query Match 21.4%; Score 138.6; DB 10; Length 1490;
 Best Local Similarity 56.7%; Pred. No. 7,9e-34;
 Matches 327; Conservative 0; Mismatches 229; Indels 21; Gaps 3;

[illegible]

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2538  CCRCCAGGCTGAGGGGGGAGCTGACAGCTCCACACAGAGCTGGAAACCTC 267
      333  TCTGACAGCTC 344
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      2658  ACTGACACACCC 2669

RESULT 12
US-09-815-342-7698
: Requester: 7698
: Patent No. US/09/00155942
: GENERAL INFORMATION:
: APPLICANT: Haseelbeck, Robert
: APPLICANT: Olsen, Karl D.
: APPLICANT: Olsen, Karl D.
: APPLICANT: Wall, Daniel
: APPLICANT: Trawick, John D.
: APPLICANT: Carr, Grant J.
: APPLICANT: Haseelbeck, Robert T.
: APPLICANT: Xu, H. Howard
: TITLE OF INVENTION: Identification of Essential Genes in
: TITLE OF INVENTION: Prokaryotes
: TITLE OF INVENTION: Prokaryotes
: FILING DATE: 09/09/2009 US/09/015,242
: CURRENT APPLICATION NUMBER:

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1	PRIOR APPLICATION NUMBER: 60/191,078
2	PRIOR FILING DATE: 2000-03-22
3	PRIOR PUBLICATION NUMBER: 2006,848
4	PRIOR PUBLICATION DATE: 2000-05-23
5	PRIOR FILING DATE: 2000-05-23
6	PRIOR APPLICATION NUMBER: 60/207,777
7	PRIOR FILING DATE: 2000-05-26
8	PRIOR APPLICATION NUMBER: 60/242,578
9	PRIOR FILING DATE: 2000-10-23
10	PRIOR PUBLICATION NUMBER: 2007,625
11	PRIOR FILING DATE: 2001-11-27


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* 47651 48350: contig of 700 bp in length
* 48351 48450: gap of 100 bp in length
* 48451 49148: contig of 698 bp in length
* 49149 49248: gap of 100 bp in length
* 49249 50061: contig of 812 bp in length
* 50062 50741: contig of 680 bp in length
* 50742 50821: gap of 100 bp in length
* 50822 51667: gap of 845 bp in length
* 51668 51677: gap of 100 bp in length
* 51678 52400: contig of 723 bp in length
* 52401 52500: gap of 100 bp in length
* 52501 52525: contig of 25 bp in length
* 52526 53274: contig of 745 bp in length
* 53275 53974: contig of 649 bp in length
* 53975 54074: gap of 100 bp in length
* 54075 54781: contig of 707 bp in length
* 54782 55008: contig of 227 bp in length
* 55009 55708: gap of 100 bp in length
* 55709 56426: contig of 718 bp in length
* 56427 57246: gap of 819 bp in length
* 57247 57344: gap of 100 bp in length
* 57345 58051: contig of 707 bp in length
* 58052 58151: gap of 100 bp in length
* 58152 58801: contig of 649 bp in length
* 58802 58801: contig of 709 bp in length

Query Match
Best Local Similarity 99.3%; Pred. No. 2.7e-16; Length 66980;
Matrix 133, Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Oy 242 CCCTCTCTTCCTGCAGAAAGTCCCTCCCTGGCGGAGTTCGTCCCAAGGGTTCCTCGA 301
Db 63986 CCCTCTCTTCCTGCAGAAAGTCCCTCCCTGGCGGAGTTCGTCCCAAGGGTTCCTCGA 63944
Oy 302 AGAATCTCTGGAGGCGGAGTCTCTGACCGAGGAGTCTCTGAGCTGTGAGAGCC 361
Db 63945 AGAATCTCTGGAGGCGGAGTCTCTGACCGAGGAGTCTCTGAGCTGTGAGAGCC 64004
Oy 362 GCACGACCCCGAGAG 375
Db 64005 GCACGACCCCGAGAG 64018

RESULT 12
AC011796/6
DEFINITION Homo sapiens clone RP11-2089, LOW-PASS SEQUENCE SAMPLING.
ACCESSION AC011796
VERSION AC011796.4 GI:12543842
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
Birnbaum, B., Linton, L., Nusbam, C. and Lander, E.
Homo sapiens, clone RP11-2089
Unpublished (to 66980)
Birnbaum, B., Linton, L., Nusbam, C., Lander, E., Allen, N., Anderson, M.,
Baldwin, J., Barna, N., Berkley, R., Boguslavsky, L., Bouckgaert, B.,
Brown, A., Casale, A., Colangelo, M., Collins, S., Collymore, A.,
Foster, P., D'Amico, R., Dwyer, K., Donnelly, M., Donnell, L., Doyle, M.,
Galligan, J., Gardy, N., Grant, G., Hagg, B., Haisfield, J., Horton, L.,
Holland, J.C., Johnson, S., Jones, C., Kann, L., Karst, A., Klein, J.,
Mehrotra, J., Lieu, C., Locke, K., MacDonald, P., Marquie, N.,
Morris, J., Naylor, J., Norman, C., O'Connell, J., O'Connell, J.,
Peterson, K., Pollara, V., Riley, R., Roy, A., Santoro, R., Savory, P.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,

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Teasdale, S., Birrell, A., Vassiliev, N., Vo, A., Wheeler, J., Wu, X.,
Wang, Y., Zimmer, A. and Zody, M.
Direct Submission
Submitted (15-NOV-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker.
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WTER
Web site: http://www-seq.wi.mit.edu
Contract: sequence_submissions@genome.wi.mit.edu
Contract project: 09-936-680-4
Center clone name: 20_H_9

***** NOTE: This record contains 83 individual
contigs. Runs of N are used to separate the reads
and the order in which they appear is completely
arbitrary. Low-pass sequence sampling is useful for
identifying repeats, but it is not possible to resolve
overlap relationships among clones to be deduced.
However, it should not be assumed that this clone
will be sequenced to completion. In the event that
the sequence is updated, the accession number will
be preserved.

* 1 683: contig of 683 bp in length
* 684 783: gap of 100 bp in length
* 784 1588: contig of 805 bp in length
* 1589 2297: contig of 708 bp in length
* 2298 2396: gap of 100 bp in length
* 2397 3101: contig of 705 bp in length
* 3102 3216: contig of 115 bp in length
* 3217 4016: gap of 100 bp in length
* 4017 4737: contig of 721 bp in length
* 4738 5557: gap of 820 bp in length
* 5558 5657: gap of 100 bp in length
* 5658 6372: contig of 715 bp in length
* 6373 7154: gap of 781 bp in length
* 7155 7255: gap of 100 bp in length
* 7256 7257: contig of 702 bp in length
* 7258 8077: gap of 100 bp in length
* 8078 8774: gap of 100 bp in length
* 8775 9577: contig of 704 bp in length
* 9578 9677: gap of 100 bp in length
* 9678 10492: contig of 810 bp in length
* 10493 11179: contig of 687 bp in length
* 11180 11279: gap of 100 bp in length
* 11280 11384: contig of 705 bp in length
* 11385 12791: contig of 707 bp in length
* 12792 12891: gap of 100 bp in length
* 12892 13600: contig of 705 bp in length
* 13601 14409: contig of 805 bp in length
* 14410 14509: gap of 100 bp in length
* 14510 15221: contig of 712 bp in length
* 15222 15231: gap of 100 bp in length
* 15232 16126: gap of 100 bp in length
* 16126 16822: contig of 697 bp in length
* 16823 17221: contig of 100 bp in length
* 17222 17721: gap of 100 bp in length

```

* 17722 18423: contig of 703 bp in length
* 18424 18523: gap of 100 bp
* 18524 19411: contig of 718 bp in length
* 19411 19456: gap of 100 bp
* 19456 20056: contig of 715 bp in length
* 20056 20156: gap of 100 bp
* 20157 20870: contig of 714 bp in length
* 20870 21571: contig of 707 bp in length
* 21571 21672: contig of 100 bp
* 21672 22480: contig of 709 bp in length
* 22480 22581: contig of 100 bp
* 22581 23393: contig of 711 bp in length
* 23393 23493: gap of 100 bp
* 23493 24093: contig of 702 bp in length
* 24093 24193: gap of 100 bp
* 24193 25017: contig of 710 bp in length
* 25017 25272: gap of 100 bp
* 25272 25635: gap of 100 bp
* 25635 27334: contig of 699 bp in length
* 27334 28331: contig of 698 bp in length
* 28331 28832: contig of 100 bp
* 28832 29026: gap of 100 bp
* 29026 29758: contig of 732 bp in length
* 29758 30567: contig of 708 bp in length
* 30567 31368: contig of 702 bp in length
* 31368 31468: gap of 100 bp
* 31468 32081: gap of 100 bp
* 32081 32884: gap of 100 bp
* 32884 33081: contig of 698 bp in length
* 33081 33795: gap of 100 bp
* 33795 33899: gap of 100 bp
* 33899 34734: contig of 736 bp in length
* 34734 35533: gap of 100 bp
* 35533 36253: gap of 100 bp
* 36253 36353: contig of 720 bp in length
* 36353 37079: gap of 100 bp
* 37079 37893: contig of 726 bp in length
* 37893 37993: contig of 714 bp in length
* 37993 38700: gap of 100 bp
* 38700 39506: contig of 707 bp in length
* 39506 40316: contig of 711 bp in length
* 40316 41133: contig of 715 bp in length
* 41133 41233: gap of 100 bp
* 41233 41940: contig of 708 bp in length
* 41940 42039: gap of 100 bp
* 42039 42749: contig of 707 bp in length
* 42749 43555: contig of 707 bp in length
* 43555 44369: gap of 100 bp
* 44369 45171: contig of 703 bp in length
* 45171 45271: gap of 100 bp
* 45271 45722: contig of 672 bp in length
* 45722 46044: contig of 100 bp
* 46044 46750: gap of 100 bp
* 46750 46850: contig of 701 bp in length

Query Match
Best Local Similarity 100.0%, Pred No. 4, 2e-06, Length 6590,
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 302 AGAGATGAGGCGCGCGCTGTTACGAGCGAGATCTCTGAGACGCGAGACCC 361
Db 49350 AGAGATCTGAGGCGCGCGCTGTTACGAGCGAGATCTCTGAGACGCGAGACCC 361

QY 362 GCGCGCGCGCGAG 375
Db 49350 GCGCGCGCGCGAG 375

QY 48290 GCGCGCGCGCGAG 48277
Db 49350 GCGCGCGCGCGAG 48277

RESULT 13
PM1286G/c
LOCUS PM1286G
DEFINITION Penicillium marneffei STS, clone pm1286.g, sequence tagged site.
ACCESSION AF644346
VERSION 1
KEYWORDS STS
SOURCE Penicillium marneffei
ORGANISM Penicillium marneffei
REFERENCE 1 Yuen K.Y., Fascal, G., Wong, S., Glaeser, P., Woo, P., Kunst, P., Cheung, Z., Medigue, C. and Danchin, A. (2002) The Penicillium marneffei genome. Unpublished.
JOURNAL
REFERENCE 2 (bases 1 to 521) Danchin, A. and Fascal, G.
AUTHORS Submitted (08-MAR-2002) Danchin A., HKU-Pasteur Research Centre, JOURNAL Dexter HC Wan Building 6, Sassoon Road, Pokfulam, Hong Kong
FEATURES
source 1..521
/db_xref="taxon:37127"
/db_xref="taxon:37127"
/clone="pm1286.g"
BASE COUNT 29 a 287 c 192 g 9 t 4 others
ORIGIN
Query Match 14.1%; Score 53; DB 11; Length 521;

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Db 65670 GCGGGGCGCTCCACCTCGGCTCCGAGTGTGAATTACAGGCGTGAAGCCTGCGCCGC 65611

Qy 306 ATTGAGAGGCGCGAGTCTTTCACGAGGGAATCTTTTGT 348

Db 65610 AGCTAGTGTCTGTCTATTCCTCTCGGTCTCTTCT 65568

Search completed: December 5, 2003, 20:51:01
Job time : 1572.17 secs

Human ORFX ORF2459 polynucleotide sequence SEQ ID NO:4917.

Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnarity; antiproliferative; antiparkinsonian; neurotropic; neuroprotective; immunomodulatory; thrombolytic; coagulant; vasoregulatory; antiproliferative; antiproliferative; dematological; immunosuppressive; antinflammatory; antiviral; antibacterial; antifungal; antihemetic; antihypertensive; neurodegenerative disease; cancer; proliferative disorder; hypertension; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; allergic rhinitis; chronic urticaria; autoimmune disorder; asthma; allergy; aplastic anemia; bone marrow failure; bone marrow failure; bone damage; cartilage disease; antinflammatory disease; coagulation; thrombosis; contraceptive; ss.

Homo sapiens.

XX DB 285 CTTGGCCCAACAGTGTGGGGCCAGGGGCTCCCGGGGGGGGATCTGGAGAGAGAGGCC 226

XX QY 105 CTGAGCCGCGCGAGCGCGCGCGCGAGCGGCTGATCGCTCCCTCGAATCGGGAGGTC 164

XX DB 225 CTTCTCGGCGAGCGAC 166

XX QY 165 CATTGGGGGCTCTTAGGGGCGCAAGGCCCCACCGCGCTCCAAAAGCTCCAGGGGCTCCG 224

XX DB 165 CAGGCGGAAAGAGATGGGGCGCGCTTGGCGCGGCTCTCGCGCCCGAGCTGGGGCGCGGGCCCC 106

XX QY 225 CAGGCGGAAAGAGATGGGGCGCGCTTGGCGCGGCTCTCGCGCCCGAGCTGGGGCGCGGGCCCC 244

XX DB 105 CTGGTGGCCCGCGAGAGGTC 86

Search completed: December 5, 2003, 17:55:06
Job time : 143.507 secs

W0200058473-A2.

05-OCT-2000.

31-MAR-2000; 2000WO-US08621.

31-MAR-1999; 99US-0127607.

02-APR-1999; 99US-0127607.

05-APR-1999; 99US-0127728.

30-MAR-2000; 2000US-0540763.

(CURA)- CURAGEN CORP.

Shimkets RA, Leach W;

WPI. 2000-502452/57.

P-FSDB; A582459.

Novel nucleic acids and peptides derived from open reading frame X,
useful for treating e.g. cancers, proliferative disorders,
neurodegenerative disorders and cardiovascular disease -

Claim 5; Page 4092-4093; 5507pp; English.

ACT7606 encodes the proteins given in A5840217 to A584397,
which represent the human ORFX open reading frame 1 to 16. The
sequences have activities such as: cytostatic; hepatotropic; vulnarity;
antiproliferative; antiparkinsonian; neurotropic; neuroprotective;
immunomodulatory; thrombolytic; coagulant; vasoregulatory; antiproliferative;
dematological; immunosuppressive; antinflammatory; antiviral;
antibacterial; antihemetic; antihypertensive; neurodegenerative disease;
cancer; proliferative disorder; hypertension; cardiovascular disease;
diabetes mellitus; hypothyroidism; SCID; AIDS; infection; allergic
rhinitis; chronic urticaria; autoimmune disorder; asthma; allergy;
aplastic anemia; bone marrow failure; bone marrow failure; bone damage;
cartilage disease; antinflammatory disease; coagulation; thrombosis;
contraceptive; ss.

Sequence 1544 BP; 209 A; 565 C; 499 G; 271 T; 0 other;

Query Match 10.2%; Score 38.4; DB 21; Length 1544;
Best Local Similarity 49.5%; Pred. No. 3.4;
Patterns 29; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

45 GCAGGGGGCGGAGTGGAGTCTCCGGGGGGGGGAGGCGACTCTCTGGTG 104

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Inc.

QM nucleic - nucleic search, using aw model

Run on: December 5, 2003, 17:08:07, Search time 1108.64 Seconds
8221.015 Million cell updates/sec

Title: US-09-936-680-4_COPY_1_375

Request score: 1 cccctccctccgagtcgagc.....gagcgcgcagccocagaag 375

Sequence: 1 cccctccctccgagtcgagc.....gagcgcgcagccocagaag 375

Scoring table: IDENTITY_MUC Gapup 10.0, Gapext 1.0

Searched: 2761392 seqs, 1215228056 residues 4556294

Total number of hits satisfying chosen parameters: 4556294

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Maximum Match 08

Maximum Match 100%

Listing first 45 summaries

Database : EST *

1: em estab.*

2: em estab.*

3: em estab.*

4: em estab.*

5: em estab.*

6: em estab.*

7: em estab.*

8: em estab.*

9: em estab.*

10: gD est2.*

11: gD htc.*

12: gD est3.*

13: gD est4.*

14: gD est5.*

15: em estfun.*

16: em estfun.*

17: em g88 hum.*

18: em g88 hum.*

19: em g88 vrt.*

20: em g88 vrt.*

21: em g88 fun.*

22: em g88 fun.*

23: em g88 mus.*

24: em g88 pro.*

25: em g88 rod.*

26: em g88 rod.*

27: em g88 vrt.*

28: gD g881.*

29: gD g882.*

SUMMARIES

Result	No.	Score	Query	Match	Length	ID	Description
1	213	8	57.0	972	13	B0068875	AL066051 Droso
2	213	8	57.0	972	13	B0068875	AL066051 Droso
3	59	4	15.8	1103	13	BX403654	AL066051 Droso
4	59	4	15.7	935	29	CNS006XK	AL066051 Droso

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

C	5	53.8	14.3	1101	29	CNS00397	AL063912 Droso
C	6	53.6	14.3	982	13	BX415111	BX415111
C	7	53.4	14.2	1603	29	AG050136	AG050136 Pan trogl
C	9	52.8	14.1	1201	9	AL538546	AL538546 AL538546
C	10	51.8	13.8	935	29	CNS006XK	AL066051 Droso
C	11	51.6	13.8	925	29	CNS0091P	AL066051 Droso
C	12	50.6	13.5	804	13	BX425573	BX425573
C	13	50.6	13.5	804	13	BX425573	BX425573
C	14	50.6	13.5	925	29	CNS0091P	AL063013 Droso
C	15	50.6	13.5	1188	13	BX371097	BX371097
C	16	50.6	13.5	1188	13	BX371097	BX371097
C	17	50.6	13.5	888	12	BG305972	BG305972
C	18	49.6	13.2	932	29	CNS00720	AL066742 Droso
C	19	49.4	13.2	1269	12	BH807701	BH807701 AGENCOURT
C	20	49.2	13.1	1061	13	BX312446	BX312446
C	21	49.2	13.1	1061	13	BX312446	BX312446
C	22	48.8	13.0	1144	13	BX415926	BX415926
C	23	48.6	13.0	970	13	BUS36852	BUS36852 AGENCOURT
C	24	48.6	13.0	1000	13	BX407619	BX407619
C	25	48.6	13.0	1000	13	BX407619	BX407619
C	26	48.6	13.0	1000	13	BX407619	BX407619
C	27	48.4	12.9	1179	13	BX425030	BX425030
C	28	48.2	12.9	956	13	BUS01227	BUS01227 AGENCOURT
C	29	48.2	12.9	966	13	BUS01227	BUS01227 AGENCOURT
C	30	48.2	12.9	1171	12	CNS07241	CNS07241
C	31	48.2	12.8	1171	12	BH914930	BH914930 AGENCOURT
C	32	47.8	12.7	873	29	AG043471	AG043471 Pan trogl
C	33	47.8	12.7	873	29	AG043471	AG043471 Pan trogl
C	34	47.8	12.6	873	29	CNS0151J	CNS0151J
C	35	47.4	12.6	1057	13	BX349688	BX349688
C	36	47.2	12.6	377	10	BG361509	BG361509 gB60411.Y
C	37	47.2	12.6	732	28	A2196033	A2196033 SP_1031_A
C	38	47.2	12.6	732	28	A2196033	A2196033 SP_1031_A
C	39	46.2	12.5	1048	12	BG832371	BG832371
C	40	46.8	12.5	1048	13	B0073900	B0073900 AGENCOURT
C	41	46.8	12.5	1138	13	BX371097	BX371097
C	42	46.6	12.4	442	28	BH727222	BH727222 SALK_0060
C	43	46.6	12.4	442	28	BH727222	BH727222 SALK_0060
C	44	46.6	12.4	1136	13	BX466909	BX466909
C	45	46.4	12.4	626	29	CNS022N9	AL221166 Tetradon

ALIGNMENTS

AL534136 1201 bp MENA linear EST 12-MAY-2003
CS0DP005Y102 5-PRIME, MENA sequence.

AL534136.2 GI.30539643

EST.

ORGANISM

Human sapiens (human)

Human sapiens

Human sapiens

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 1201)

Li, W.-B., Gruber, C., Jessee, J., and Polayes, D.

Unpublished

On Feb 13, 2001 this sequence version replaced gi1297629.

Contact: Genoscope

Genoscope, Centre National de Sequencage

Genoscope, Centre National de Sequencage

Shall: seq@genoscope.cns.fr, Web : www.genoscope.cns.fr

Invitrogen. This sequence belongs to sequence cluster 6147.r For

http://www.genoscope.cns.fr/cluster, see

http://www.genoscope.cns.fr/cluster, see

Feng Liang Email : fliang@life.technet.com URL :

collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the *Drosophila* melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org>. The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Onoegawa and Aaron Mamoer in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCR-98 and was constructed by partial

COMMENT
- Web : www.genoscope.cns.fr/
determination of this BAC-IR?
collaboration with the Berkeley Drosophila genome project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see <http://www.fruitfly.org> The BDGP Drosophila
melanogaster BAC library was prepared by Kazuhiro Oosawa and
Anton Mamonov in Pieter de Jong's laboratory in the Department of


```

BASE COUNT      226 a    205 c    283 g    57 t    229 others
ORIGIN
Query Match      14.28; Score 53.41; DB 13; Length 1000;
Best Local Similarity 22.98; Prd No. 0.024;
Matches 58; Conservative 98; Mismatches 97; Indels 0; Gaps 0;
Qy 1 GCGCTGCTTCGAGCTGAGCTTACCTGCGGCGAAGCGAGCGCGCGCCATGCG 60
Db 686 CCCCCCTTCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT 127
Qy 61 AGCTGCGAGTGTGCGGCGGAGCGAGCGACGTCGCTGCTGCTGCTGCTGCTGCT 150
Db 624 CAGTCCGCTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 126
Qy 121 CGCGCGCGCGAGCGCGGCTGATCGCTGCTTCGACATCGGAGGCTCCGCTGCTTGA 180
Db 566 SSBTBSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS 507
Qy 181 GCGCGAAGAGCGAGCTCGGCTCGAAGAGCTTCGAGGCTTCCGCGAGCGAGTGTG 240
Db 506 GGGGCGCGACGCGTGGTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT 447
Qy 241 GCGCTGCTTCGCG 253
Db 446 GGGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 434

RESULT 8
LOCUS 36/c
DEFINITION AG060136 693 bp DNA linear GSS 03-NOV-2001
ACCESSION AG060136
VERSION AG060136.1 GI:16611366
KEYWORDS
SOURCE Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
ORGANISM
Pan troglodytes (chimpanzee)
Pan troglodytes
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T.,
Totoki, Y., Matanabe, H. and Sakaki, Y.
Unpublished sequences of Library PTB
2 (bases 1 to 693)
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T.,
Totoki, Y., Matanabe, H. and Sakaki, Y.
Submitted (02-AUG-2001) Aono Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suhraro-cho, Tsukuba-Ku, Yokohama, Kanagawa 230-0045, Japan
Tel:81-45-503-9111 Fax:81-45-503-9170
http://hgp.igc.riken.go.jp/
Clones are derived from the chimpanzee BAC library PTB this BAC end
was generated during the Rad process and may have higher chance of
chimeric tracking errors.
Clones Sequencing: -21M13
LIBRARY
Vector 1 : pMS145
Vector 2 : pMS145
R Site 1 : SacI
R Site 2 : SacI
FEATURES
source
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-047116.F"
/sex="male"
/sex="male"
/clone_lib="PTB Chimpanzee Male BAC Library"
99 a 344 c 160 g 60 t 30 others

BASE COUNT      99 a    344 c    160 g    60 t    30 others
ORIGIN
Query Match      14.11; Score 52.8; DB 9; Length 1201;
Best Local Similarity 49.41; Prd No. 0.029;
Matches 131; Conservative 0; Mismatches 134; Indels 0; Gaps 0;
Qy 28 GGGCGAAGCGAGCGAGCGAGCGAGCGAGCGAGCTGAGCTGAGCTGCGGCGCGGCG 87
Db 647 GGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 568
Qy 88 GCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 147
Db 587 GCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 528
Qy 148 CTCGAGACTGCGGAGGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 207
Db 527 GGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 468
Qy 208 AGCTCCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 267
Db 467 TGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 267
Qy 268 CTGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 292
Db 407 GCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 383

RESULT 9
LOCUS 1201 bp mRNA linear EST 31-MAY-2003
DEFINITION AL538546 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
ACCESSION AL538546
VERSION AL538546.2 GI:31263136
KEYWORDS EST.
SOURCE Homo sapiens (human)
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Unpublished
Full-length cDNA libraries and normalization
On Feb 13, 2001 this sequence version replaced gi:12602039.
Contact: Genoscope
National de Sequences
BP 131 91066 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Genoscope, a French Genomic Sequencing Cluster 3991: For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/crawler.cgi?seq=CS09F024D80NPF1cluster=399.9. Contact :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Harvey Avenue Genoscope sequence ID : CS09F024D80NPF1.
FEATURES
source
Location/Qualifiers
1..1201
/mol_type="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS09F024X718"
/clone_lib="Homo sapiens FETAL BRAIN"
/dev stage="fetal"
/clone_lib="Homo sapiens FETAL BRAIN"
/notes="Organ: brain; Vector: pMS145; 1st strand cDNA
was primed with a NotI-oligo dT primer. Five prime and
three prime ends double stranded cDNA were sequenced
cloned into the Not I and KpnI sites of the pMS145 6
vector. Library was not normalized."
BASE COUNT      247 a    211 c    314 g    171 t    258 others
ORIGIN
Query Match      14.11; Score 52.8; DB 9; Length 1201;

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Db          573 CTTNCCCT 581
|||||
CNS0091P    925 bp    DNA    linear    GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence T873 end of BAC #
EACH19015 of RPCI-98 library from Drosophila melanogaster (fruit
fly) genomic survey sequence.
ACCESSION   AL053033
VERSION     GSS
KEYWORDS    Drosophila melanogaster (fruit fly)
ORGANISM    Drosophila melanogaster
            BUKARYOTA; METAZOA; ARTHROPODA; HEXAPODA; INSECTA; PTERYGOTA;
            NEOPTERA; ENDOPTERYGOTA; DIPTERA; BRIDCHYOTERA; MUSCOPHORA;
            DROSOPHILIDAE; DROSOPHILA.
            (bases 1 to 925)
REFERENCE   Direct Substitution
AUTHORS     Genoscope
JOURNAL     Genoscope - Centre National de Sequencage ;
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqfr@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BAC-end sequence was determined using the BACs. For further information
            please see http://www.fruitfly.org the BDGP Drosophila
            melanogaster BAC library was prepared by Kazuo Ooegawa and
            colleagues at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y4; cn bw sp. The same strain used for the BDGP's
            library was used for the construction of the BAC library. The library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES     1. contigs
            source
            /organism="Drosophila melanogaster"
            /mol_type="genomic DNA"
            /db_xref="taxon:7227"
            /clone="BACR19015"
            /note="end : T873"
BASE COUNT   120 a 61 c 61 g 172 t 511 others
ORIGIN
Query Match          12.5%; Score 50.6; DB 29; Length 925;
Best Local Similarity 13.5%; Pred. No. 0.11;
Matches              150; Mismatches 135; Indels 0; Gaps 0;
QY 5 CTTCTCGAGCTAGCTTACCTCGGCGCAAGAGGAGGAGCGGGCGGAGTGAAGC 64
DB 572 CTTCTCGAGCTAGCTTACCTCGGCGCAAGAGGAGGAGCGGGCGGAGTGAAGC 631
QY 65 TGAAGTTCGGGGTGGGGGAGGAGGAGTCTGCTGCTGAGCGCCGCGAGAGGCG 124
DB 62 GSSGCGGSSGSSSTGSSSTGSSGSSGSSGSSSTGSSSTGSSGSSGSSGSSG 691
QY 125 GCGGAGGAGTTCGAGTCTGCTGAGCTGGGAGGAGTCTGAGTGGTCTGATAGGCG 184
DB 692 TGTSTSSSSSTSTSSSTSSSTSSSTSSSTSSSTSSSTSSSTSSSTSSSTSS 751
QY 185 CAAAGCCCAACCGAGCTCAAAAGCTCCAGAGGCTCCCGAGGACGAGCTGTGCC 244
DB 742 SYSSCTTCGCTGAGAGAGTCCGCTGSSSTSSSTSSSTSSSTSSSTSSSTSS 244
QY 215 TTTCTTCGCTGAGAGAGTCCGCTGSSSTSSSTSSSTSSSTSSSTSSSTSS 811
DB 812 CTTCTTCGCTGAGAGAGTCCGCTGSSSTSSSTSSSTSSSTSSSTSSSTSS 871

```

```

Db          305 AMTCTGAGGCGCGAGCTCTTTCACGAGGATC 339
872 GSSGSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS 906
|||||
RESULT 15
EX371097/c
DEFINITION
EX371097 Homo sapiens PLACENTA, COT 25-NORMALIZED Homo sapiens CDNA
clone, CS001035V15 5-PRIME, mRNA sequence.
ACCESSION   EX371097.1
VERSION     EX371097.1
KEYWORDS    Homo sapiens
ORGANISM    Homo sapiens (human)
            BUKARYOTA; METAZOA; CHORDATA; CRANIATA; VERTEBRATA; EUTELEOSTOMI;
            MAMMALIA; PRIMATES; PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
            (bases 1 to 1398)
REFERENCE   Li, W.B., Gruber, C., Jesses, J. and Polayes, D.
            Full-length cDNA libraries and normalization
            Amplification of cDNA libraries
            Genoscope - Centre National de Sequencage
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email : seqfr@genoscope.cns.fr; Web : www.genoscope.cns.fr
            Invitrogen, Contact : Feng Liang Email : fliang@lifestech.com URL :
            http://fulllength.invitrogen.com/Invitrogen Corporation 1600
            Parady Avenue Genoscope sequence ID : CS0BAH0142E01QP1.
            Location/Qualifiers
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /tissue="Placenta"
            /clone="PLACENTA COT 25-NORMALIZED"
            /note="1st strand cDNA was primed with a NOTI-oligo(dT)
            primer and the second strand was synthesized using a
            primered with poly(I) and cloned into the NotI and EcoR
            sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT   235 a 273 c 215 g 150 t 327 others
ORIGIN
Query Match          31.5%; Score 90.6; DB 13; Length 1198;
Best Local Similarity 33.3%; Pred. No. 0.11;
Matches              26; Mismatches 104; Indels 0; Gaps 0;
QY 28 GGGCGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTTCGCGGTG 87
DB 533 GGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 474
QY 88 GGCACGACTGCTCGCTGGCTGAGCGCGGCGGAGCGCGGCGGAGCGGCTGATCGCTC 147
DB 473 GGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 414
QY 149 CTCGAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 207
DB 413 SCSSAAAAAASASSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS 354
QY 208 AGCTCGACGAGCTCTCGCGGCGCGGCTGCTGGCGCTCTTCTGGTGTGAGAAATCGCC 267
DB 353 GSSGSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS 294
QY 266 CTT 270
DB 293 CTT 291

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Search completed, December 5, 2003, 22:55:28
 Job time : 1112.64 secs

SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 19
 LENGTH: 38506
 TYPE: DNA
 ORGANISM: Streptomyces venezuelae
 US-09-657-440-15

Query Match 9.7%; Score 36.2; DB 4; Length 38506;
 Best Local Similarity 45.6%; Pred. No. 2.5; Indels 0; Gaps 0;
 Matches 105; Conservative 0; Mismatches 153;
 Qy 91 CTCTCTGCTGCTGAGCGCGCGAGCGCGCGAGCGCGTGTGCTGCTCTCTCGA 152
 Db 3393 CTGCGAGCGTGAAGCTGCTGGGCTGTGCGAGTCCGAGTCACTCCCTCAGCTC 3334
 Qy 153 ATGCGGAGCTCAGCGGCTCTTAGCGCGAAGCGCCACCGGCTCCAAAGCTC 212
 Db 3333 CAGCGCGCGCTGCGAGACTCGAGATCGGCTCCCGCCGCGCAGCGCGCA 3274
 Qy 213 CAGGCGCTCCCGAGCGACGGGTGCTGCGCCCTCTCTGTGAGAAATGCGCCCTGG 272
 Db 3273 CAGCTCTCTCGCGCGAGCGACCCCGACCGCGGAGCGGCGGCGCATGCGCC 3214
 Qy 273 GGGCGCTCTCCCGCAGGGTTCCTCGAAGAAATCGAGAGCGCGAGCTCTGACGA 332
 Db 3213 CGGCTGTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGGTTGC 3154
 Qy 333 GGGAACTCTCTGTGTAGCTGTGAAGCGCGCGCGCGCGCA 373
 Db 3153 CGCGCGCTCTCCCGTGCAGCGAGGAGCTGCTCTCGCA 3113

RESULT 8
 US-09-252-991A-198
 Sequence 198; Application US/0925991A
 Patent No. 6043088
 GENERAL INFORMATION:
 APPLICANT: Marc J. Rubenfield et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ORGANISM: Pseudomonas aeruginosa
 FILE REFERENCE: 107196.136
 CURRENT APPLICATION NUMBER: US/09/282.991A
 CURRENT FILING DATE: 1999-02-18
 PRIOR FILING DATE: 1998-02-18
 PRIOR APPLICATION NUMBER: US 60/094,190
 PRIOR FILING DATE: 1998-07-27
 NUMBER OF SEQ ID NOS: 33142
 SEQ ID NO 1020
 LENGTH: 1020
 TYPE: DNA
 ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-198

Query Match 9.6%; Score 36; DB 4; Length 1020;
 Best Local Similarity 47.7%; Pred. No. 1.8; Indels 0; Gaps 0;
 Matches 105; Conservative 0; Mismatches 115;
 Qy 12 GAGCTGAGCTTACCCTGGCGCAACAGCGAGCGAGCGGCGCGAGCTGAGTGT 71
 Db 72 GCGGGTGTGGCGGAGCGAGCTGCTGTGCTGCTGAGCGCGCGCGCGCGAGCG 131
 Qy 72 GCGGGTGTGGCGGAGCGAGCTGCTGTGCTGCTGAGCGCGCGCGCGCGAGCG 131
 Db 784 GCGGGGCGCTGAGCGCTCTCTGTCTCTCTCGGAGACTGTTCAGTGTGCGG 843
 Qy 132 GCGCGTATGGCTCTCTCGACTCGGGAGGCTGCTGGGGTTCGCTTAGGCGCC 191
 Db 844 CGGCTGATATATCACTCGGTGATCGGGATATCCCGGCGCTTCGCGATGATG 903
 Qy 192 CCACCGGCTCCAAAGCTCCAGGAGCTCCAGGAGCTCCCGACGAC 231
 Db 304 ACCGGTGTGCTGCTGATTGAAGGGGATCAAGCGGCGC 943

RESULT 9
 US-08-445-515-52/c
 Sequence 52; Application US/08445515
 Patent No. 6043088
 GENERAL INFORMATION:
 APPLICANT: Bookstein, Robert
 APPLICANT: Isaac, William B.
 TITLE OF INVENTION: Prostete/Colon Tumor Suppressor
 ORGANISM: Gene Located on Human Chromosome 8
 NUMBER OF SEQUENCES: 59
 CORRESPONDENCE ADDRESS:
 STREET: 4370 La Jolla Village Drive, Suite 700
 CITY: San Diego
 STATE: California
 ZIP: 92122
 COUNTRY: USA
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 SOFTWARE: PatentIn Ver. 2.0
 CURRENT APPLICATION DATA: Version #1.0, Version #1.25
 APPLICATION NUMBER: US/08/445-515
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Campbell, Cathryn A.
 REGISTRATION NUMBER: 31.815
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 535-9001
 TELEFAX: (619) 535-8949
 INSURANCE: 52
 SEQUENCE CHARACTERISTICS: 52
 LENGTH: 1342 base pairs
 TYPE: nucleic acid
 TOPOLOGY: linear
 US-08-445-515-52

Query Match 9.5%; Score 35.9; DB 3; Length 1342;
 Best Local Similarity 47.9%; Pred. No. 2;
 Matches 103; Conservative 0; Mismatches 112; Indels 0; Gaps 0;
 Qy 20 CTTACCTGTGGTGAACGACGACGAGCGCGCTGATGTGACTGTGCTCGGATG 79
 Db 279 CTTCTCCCGAGCTGATGACGACGACGACGACGACGACGACGACGACGACG 220
 Qy 80 GCGCGGCGCGCTGCTGTGCTGTGCTGAGCGCGCGCGCGCGCGCGCGCGTGA 119
 Db 219 GCGCGGCG 160
 Qy 140 TCGCTCTCTCTGAACTGGGAGGCTCGTGGGCTGCTGTAGGCGCGGAGCGCG 199
 Db 159 ATCCGCGCGGCGGCTGCTCTCTCTGCGCGCGCGCGCGCGCGCGCGCGCG 100
 Qy 200 GTCCGAAAGCTCTCCAGGCGCTCCCGAGGACCGG 214
 Db 99 GACCCGCGCTCTCCGCGCTCTCCGCGCGCGCGCGCGCGCGCGCGCGCG 65

RESULT 10
 US-08-445-515-52/c
 Sequence 53; Application US/08445515
 Patent No. 6043088
 GENERAL INFORMATION:
 APPLICANT: Bookstein, Robert
 APPLICANT: Isaac, William B.
 TITLE OF INVENTION: Prostete/Colon Tumor Suppressor
 ORGANISM: Gene Located on Human Chromosome 8

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1  TITLE OF INVENTION: Recombinant Megalomicin Biosynthetic
2  TITLE OF INVENTION: Genes and Uses Thereof
3  CURRENT APPLICATION NUMBER: US/09/679,279
4  CURRENT FILING DATE: 2000-10-04
5  PRIOR APPLICATION NUMBER: US 60/156,305
6  PRIOR FILING DATE: 2000-03-17
7  PRIOR APPLICATION NUMBER: US 60/190,024
8  PRIOR FILING DATE: 2000-03-17
9  NUMBER OF SEQ ID NOS: 34
10 SOFTWARE: FastSeq for Windows Version 4.0
11 SEQ ID NO: 1
12 LENGTH: 47981
13 TYPE: DNA
14 ORGANISM: Micromonospora megalomica
15 NAME/KEY: CDS
16 LOCATION: (1)...(144)
17 OTHER INFORMATION: megBVI (megT), TDP-4-keto-6-deoxyglucose-2,3-dehydratase;
18 OTHER INFORMATION: SEQ ID NO: 2= translated amino acid sequence
19 NAME/KEY: CDS
20 LOCATION: (144)...(2061)
21 OTHER INFORMATION: megDVI, TDP-4-keto-6-deoxyglucose 3,4-1-isomerase,
22 OTHER INFORMATION: SEQ ID NO: 3= translated amino acid sequence
23 NAME/KEY: CDS
24 LOCATION: (2072)...(3382)
25 OTHER INFORMATION: megDII, rhodosaminyl transferase (eryCIII homolog),
26 OTHER INFORMATION: TDP-megosamine glycosyltransferase;
27 OTHER INFORMATION: SEQ ID NO: 4= translated amino acid sequence
28 NAME/KEY: CDS
29 LOCATION: (3462)...(4634)
30 OTHER INFORMATION: megDIII, mycarosyl acyltransferase, mycarose O-acyltransferase
31 OTHER INFORMATION: SEQ ID NO: 5= translated amino acid sequence
32 NAME/KEY: CDS
33 LOCATION: (4651)...(5775)
34 OTHER INFORMATION: megDII, deoxyaugar transaminase (eryCI, DmrJ homolog),
35 OTHER INFORMATION: TDP-4-keto-6-deoxyhexose 3,4-1-isomerase;
36 OTHER INFORMATION: SEQ ID NO: 6= translated amino acid sequence
37 NAME/KEY: CDS
38 LOCATION: (5822)...(6595)
39 OTHER INFORMATION: megDIII, daunosaminyl-N,N-dimethyltransferase (eryCVI homolog);
40 OTHER INFORMATION: SEQ ID NO: 7= translated amino acid sequence
41 NAME/KEY: CDS
42 LOCATION: (6592)...(7197)
43 OTHER INFORMATION: megDVI, TDP-4-keto-6-deoxyglucose 3,5-epimerase (eryBVII, dnmV hc
44 OTHER INFORMATION: SEQ ID NO: 8= translated amino acid sequence
45 NAME/KEY: CDS
46 LOCATION: (7220)...(8206)
47 OTHER INFORMATION: TDP-hexose 4-ketoreductase (eryDVI, dnmV homolog),
48 OTHER INFORMATION: TDP-4-keto-6-deoxyhexose 4-ketoreductase;
49 OTHER INFORMATION: SEQ ID NO: 9= translated amino acid sequence
50 NAME/KEY: CDS
51 LOCATION: (8206)...(9290)
52 OTHER INFORMATION: megDIII-1 (megDVI), TDP-4-keto-6-deoxy-hexose 2,3-reductase;
53 OTHER INFORMATION: SEQ ID NO: 10= translated amino acid sequence
54 NAME/KEY: CDS
55 LOCATION: (9226)...(10479)
56 OTHER INFORMATION: megDIII, mycarosyl transferase, mycarose glycosyltransferase;
57 OTHER INFORMATION: SEQ ID NO: 11= translated amino acid sequence
58 NAME/KEY: CDS
59 LOCATION: (10483)...(11424)
60 OTHER INFORMATION: TDP-hexose 4-ketoreductase,
61 OTHER INFORMATION: megDIII, TDP-keto-6-deoxyhexose 4-ketoreductase;
62 OTHER INFORMATION: SEQ ID NO: 12= translated amino acid sequence
63 NAME/KEY: CDS
64 LOCATION: (12181)...(22421)
65 OTHER INFORMATION: megDIII, TDP-4-keto-6-deoxyhexose 4-ketoreductase;
66 OTHER INFORMATION: SEQ ID NO: 13= translated amino acid sequence
67 NAME/KEY: misc_feature
68 LOCATION: (12505)...(13470)
69 OTHER INFORMATION: megAII, AT-L
70 NAME/KEY: misc_feature
71 LOCATION: (37660)...(38120)
72 OTHER INFORMATION: megAII, SEQ ID NO: 15= translated amino acid sequence
73
74 LOCATION: (13576)...(13791)
75 OTHER INFORMATION: megAII, ACP-L
76 LOCATION: (13791)...(15126)
77 OTHER INFORMATION: megAII, ACP-L
78 LOCATION: (13661)...(15126)
79 OTHER INFORMATION: megAII, KS1
80 NAME/KEY: misc_feature
81 LOCATION: (15127)...(16476)
82 OTHER INFORMATION: megAII, AT-L
83 NAME/KEY: misc_feature
84 LOCATION: (17155)...(17694)
85 OTHER INFORMATION: megAII, KS1
86 NAME/KEY: misc_feature
87 LOCATION: (17694)...(18207)
88 OTHER INFORMATION: megAII, ACP1
89 NAME/KEY: misc_feature
90 LOCATION: (18268)...(19548)
91 OTHER INFORMATION: megAII, KS2
92 NAME/KEY: misc_feature
93 LOCATION: (19548)...(20910)
94 OTHER INFORMATION: megAII, AT2
95 NAME/KEY: misc_feature
96 LOCATION: (21517)...(22053)
97 OTHER INFORMATION: megAII, KS2
98 NAME/KEY: misc_feature
99 LOCATION: (22318)...(22575)
100 OTHER INFORMATION: megAII, ACP2
101 NAME/KEY: CDS
102 LOCATION: (22867)...(33555)
103 OTHER INFORMATION: megAII, SEQ ID NO: 14= translated amino acid sequence
104 NAME/KEY: misc_feature
105 LOCATION: (22957)...(24237)
106 OTHER INFORMATION: megAII, KS3
107 NAME/KEY: misc_feature
108 LOCATION: (24581)...(25581)
109 OTHER INFORMATION: megAII, AT3
110 NAME/KEY: misc_feature
111 LOCATION: (26230)...(26733)
112 OTHER INFORMATION: megAII, KS3 (inactive)
113 NAME/KEY: misc_feature
114 LOCATION: (26733)...(27258)
115 OTHER INFORMATION: megAII, ACP3
116 NAME/KEY: misc_feature
117 LOCATION: (27258)...(28590)
118 OTHER INFORMATION: megAII, KS4
119 NAME/KEY: misc_feature
120 LOCATION: (28897)...(29931)
121 OTHER INFORMATION: megAII, AT4
122 NAME/KEY: misc_feature
123 LOCATION: (29953)...(30477)
124 OTHER INFORMATION: megAII, DH4
125 NAME/KEY: misc_feature
126 LOCATION: (30477)...(32244)
127 OTHER INFORMATION: megAII, ER4
128 NAME/KEY: misc_feature
129 LOCATION: (32257)...(32799)
130 OTHER INFORMATION: megAII, KS4
131 NAME/KEY: misc_feature
132 LOCATION: (33052)...(33312)
133 OTHER INFORMATION: megAII, ACP4
134 NAME/KEY: CDS
135 LOCATION: (43271)...(43271)
136 OTHER INFORMATION: megAII, SEQ ID NO: 15= translated amino acid sequence
137 LOCATION: (33780)...(35027)
138 OTHER INFORMATION: megAII, KS5
139 NAME/KEY: misc_feature
140 LOCATION: (35385)...(36419)
141 OTHER INFORMATION: megAII, AT5
142 NAME/KEY: misc_feature
143 LOCATION: (36419)...(36604)
144 OTHER INFORMATION: megAII, KS5
145 NAME/KEY: misc_feature
146 LOCATION: (37660)...(38120)
147 OTHER INFORMATION: megAII, KS5

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1 OTHER INFORMATION: megallii, ACP5
2 NAME/KEY: misc feature
3 LOCATION: (38187)...(39470)
4 OTHER INFORMATION: megallii, KS6
5 NAME/KEY: misc feature
6 LOCATION: (39795)...(40811)
7 OTHER INFORMATION: megallii, AT6
8 NAME/KEY: misc feature
9 LOCATION: (4146)...(4496)
10 OTHER INFORMATION: megallii, KS6
11 NAME/KEY: misc feature
12 LOCATION: (42158)...(42425)
13 OTHER INFORMATION: megallii, ACP6
14 NAME/KEY: misc feature
15 LOCATION: (42585)...(43271)
16 OTHER INFORMATION: megallii, TS
17 NAME/KEY: CDS 5659)..(43344)
18 OTHER INFORMATION: megallii, ACP5
19 OTHER INFORMATION: megallii, TDP-4-keto-6-deoxyglucose 3,4-isomerase;
20 NAME/KEY: CDS 5655)..(45623)
21 OTHER INFORMATION: megallii, desoraminyl transferase, desoramine glycosyltransferase;
22 NAME/KEY: CDS 5655)..(45623)
23 OTHER INFORMATION: megallii, TDP-4-keto-6-deoxyglucose 2,3 dehydratase;
24 NAME/KEY: CDS 5655)..(45623)
25 OTHER INFORMATION: megallii, TDP-4-keto-6-deoxyglucose 2,3 dehydratase;
26 NAME/KEY: CDS 5655)..(45623)
27 OTHER INFORMATION: megallii, TDP-4-keto-6-deoxyglucose 2,3 dehydratase;
28 NAME/KEY: CDS 5655)..(45623)
29 OTHER INFORMATION: megallii, TDP-4-keto-6-deoxyglucose 2,3 dehydratase;
30 NAME/KEY: CDS 5655)..(45623)
31 OTHER INFORMATION: megallii, TDP-4-keto-6-deoxyglucose 2,3 dehydratase;
32 NAME/KEY: CDS 5655)..(45623)
33 OTHER INFORMATION: megallii, TDP-4-keto-6-deoxyglucose 2,3 dehydratase;
34 NAME/KEY: CDS 5655)..(45623)
35 OTHER INFORMATION: megallii, TDP-4-keto-6-deoxyglucose 2,3 dehydratase;
36 NAME/KEY: CDS 5655)..(45623)
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; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA

/ Mon Dec 8 11:25:47 2003

us-09-936-680-4_copy_1_375.rmpb

Page 9

Job time : 157.126 secs

1

[illegible]

1

1

1

[illegible]

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ON nucleic - nucleic search, using sw model

Run on:

December 5, 2003, 14:12:31, Search time 89.6511 Seconds
7166.298 Million cell updates/sec
(without alignments)

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Perfect score: 238

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Scoring table: IDENTITY WUC

Gapop 10.0, Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	216	90.8	4625	23	AA97864
5	216	90.8	4625	23	AA97864
6	38.6	16.2	11089	22	AAK79653
7	38	16.0	38360	24	ABQ75124
8	37.8	15.9	3768	24	ABK4794

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 Breast cancer rela
 Prostate cancer re
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 Human immune/hema
 Human immune/hema
 Rat sodium channel
 Rat sodium channel
 Human testicular a
 Human testicular a
 Human testicular a
 Human 5-lipoxygena
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 Human immune sysle
 Human ORF Polynuc
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 Mouse genomic regi
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 Human cDNA differe
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ALIGNMENTS

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XX (HUMA-) HUMAN GENOME SCI INC.
XX Rosen Ca, Barash SC, Ruben SM;
XX WPI, 2001-48232/52.
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XX Nucleic acids encoding 973 human testicular antigen polypeptides,
XX useful for preventing, diagnosing and/or treating testicular cancer -
XX
XX Disclosure; SEQ ID NO 2516; 766pp. English.
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XX The present invention provides the protein and coding sequences of 973
XX human testicular antigens, and fragments of their genomic sequences. The
XX antigens can be used in the treatment of cardiovascular, urinary system,
XX reproductive system, and gastrointestinal disorders, and particularly cancer,
XX especially testicular cancers. The present sequence is a DNA encoding a
XX protein fragment of the invention.
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DT	15-MAY-2002 (first entry)
XX	
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[illegible]

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OM nucleic - nucleic search, using sw model

Run on: December 5, 2003, 17:08:07 : Search time 703.619 seconds
8221.015 Million cell updates/sec

Title: US-09-936-680-4_COPY_1024_1261
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Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562704

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Lifting first 45 summaries

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- 8: en estro:*
- 9: gb est1:*
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pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIS

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7	41.2	17.6	322	10	BG001495
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9	40.8	17.1	941	29	CSN02DUB
10	40.2	16.9	844	29	CSN02DUB
11	39.0	16.8	611	28	BH081336
12	39.0	16.8	611	28	BH081336
13	39.0	16.8	611	28	BH081336
14	38.6	16.2	660	14	BY730622
15	38.6	16.2	1101	29	CSN05122
16	38.4	16.1	688	29	BG079943
17	38.4	16.1	688	29	BG079943
18	38.2	16.1	751	28	AQ957360
19	38	16.0	835	28	AQ748173
20	37.8	16.0	1201	9	AL564828
21	37.8	15.9	982	29	CSN05C7G
22	37.8	15.9	982	29	CSN05C7G
23	37.8	15.9	1045	29	CSN05M4G
24	37.6	15.8	436	28	AQ813992
25	37.6	15.7	155	28	AQ01381
26	37.6	15.7	155	28	AQ01381
27	37.4	15.7	542	28	BZ173993
28	37.2	15.6	505	13	BX258128
29	37.2	15.6	530	29	BZ609976
30	37.2	15.6	530	29	BZ609976
31	37.2	15.6	808	29	BX11482
32	37.2	15.6	852	29	CSN03HM2
33	37.2	15.6	1288	10	BG035459
34	37.2	15.6	384	29	AK482133
35	37	15.5	349	29	BX152709
36	37	15.5	349	29	BX152709
37	37	15.5	378	29	BX240490
38	37	15.5	640	29	BX171544
39	37	15.5	640	29	BX171544
40	37	15.5	800	13	BX701454
41	37	15.5	800	29	BX187506
42	37	15.5	833	29	BZ284733
43	36.8	15.5	713	29	BX172653
44	36.8	15.5	713	29	BX172653
45	36.8	15.5	739	29	BX200998

ALIGNMENTS

EX452112 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
CS00P023YA09 5-PRIME, mRNA sequence.
EST. GI:31024339

977 bp mRNA linear EST 22-MAY-2003
EX452112 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
CS00P023YA09 5-PRIME, mRNA sequence.
EST. GI:31024339

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Genoscope - Centre National de Sequençage
BP 91 91006 Evry cedex - France
http://www.genoscope.cns.fr
Library was constructed by Life Technologies Inc.
Invitrogen. This sequence belongs to sequence cluster 6147.r For
more information about this cluster, see
http://www.genoscope.cns.fr
http://www.genoscope.cns.fr
Contact : Peng Liang Email : fliang@lifetech.com URL
http://fulllength.invitrogen.com/ invitrogen Corporation 1600

LOCUS		4149 bp	mRNA	linear	HTC 05-DEC-2002
DEFINITION	Mus musculus ES cells cDNA, Riken full-length enriched library, clone:C30019103 Product:VOLTAGE-GATED SODIUM CHANNEL BETA-3 SUBUNIT (SODIUM CHANNEL BETA 3 SUBUNIT) homolog [Rattus norvegicus], full insert sequence.				
ACCESSION	AK049386	1 GI:26093400			
VERSION	AK049386.1				
KEYWORDS	HTC; CAP TRAPPER;				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Eukaryotic Metazoa; Chordata; Craniata; Vertebrates; Euteleostomi; Mammalia; Batartia; Rodentia; Sciurognathi; Muridae; Mus; Carnipini P. and Hayashizaki Y.				
TITLE	High-efficiency full-length cDNA cloning				
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)				
MEDLINE	93279253				
REFERENCE	2 0459536				
AUTHORS	Carnipini P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Komoto H., Okasaki Y., Muramatsu M. and Hayashizaki Y.				
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to identify novel genes for rapid discovery of new genes				
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)				
MEDLINE	20459374				
PUBMED	2049374				
REFERENCE	1 1042159				
AUTHORS	Shibata K., Itoh M., Aizawa K., Nagakura S., Saeki N., Caminici P., Komoto H., Akiyama J., Mihi K., Kitamura T., Tashiro H., Itoh M., Sumi M., Ishii Y., Nakamura S., Hazama N., Mishine T., Harada A., Yamamoto K., Matsumoto H., Sakaguchi S., Ikegami T., Washiwagi K., Yoneda S., Ishikawa K., Ogasawara K., Tanaka M., Takemura J., Okasaki Y., Muramatsu M., Inoue Y., Kita A. and Hayashizaki Y.				
TITLE	RKEN integrated sequence analysis (RISA) system -384-format				
JOURNAL	Nucleic Acids Res. 19 (11), 1757-1771 (2000)				
MEDLINE	20530911				
PUBMED	11076861				
REFERENCE	4				
AUTHORS	Arai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Aizawa K., Izawa M., Nishi K., Miyasawa K., Kondou J.Y., Fukuda S., Saito T., Ohazaki M., Gajbori T., Bono H., Kanekawa T., Saito R., Adachi K., Matsuda H., Bernheimer M., Banlov S., Casavant T., Knehl P., Lewis S., Matsui T., Nakatsuki C., King B., Kochiwa H., Quackenbush J., Schmitt L.M., Staubli F., Suzuki K., Tomita M., Wagner I., Washio T., Sakai K., Okido T., Furuno M., Aono H., Maldarelli R., Barth G., Blake D., Boffelli D., Bojunga N., Choudhury S., Fleischer C., Fujita M., Gariboldi M., Gutierrez-Castell D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Melina J., Mazzarelli J., Mombauris P.; Nordone P., Satoh K., Schombach C., Seya T., Shimizu S., Sakaki H., Sato K., Schombach C., Seya T., Shimizu S., Sakaki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Waltinger N., Winkler S., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlschütter S. and Hayashizaki Y.				
TITLE	Construction of a full-length mouse cDNA collection				
JOURNAL	Nature 409 (6821), 685-690 (2001)				
MEDLINE	21095660				
PUBMED	11217851				
REFERENCE	5				
AUTHORS	The PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.				
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs				
JOURNAL	Nature 409 (6821), 645-649 (2001)				
MEDLINE	21095660				
PUBMED	11217851				
REFERENCE	6 (bases 1 to 4149)				
AUTHORS	Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Fukuda S., Furuno M., Hanigaki T., Hara A., Hashizume Y., Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,				
LOCUS		4149 bp	mRNA	linear	EST 24-JAN-2001
DEFINITION	Mus musculus ES cells cDNA, Riken full-length enriched library, clone:C30019103 Product:VOLTAGE-GATED SODIUM CHANNEL BETA-3 SUBUNIT (SODIUM CHANNEL BETA 3 SUBUNIT) homolog [Rattus norvegicus], full insert sequence.				
ACCESSION	AK049386	1 GI:26093400			
VERSION	AK049386.1				
KEYWORDS	HTC; CAP TRAPPER;				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Eukaryotic Metazoa; Chordata; Craniata; Vertebrates; Euteleostomi; Mammalia; Batartia; Rodentia; Sciurognathi; Muridae; Mus; Carnipini P. and Hayashizaki Y.				
TITLE	High-efficiency full-length cDNA cloning				
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)				
MEDLINE	93279253				
REFERENCE	2 0459536				
AUTHORS	Carnipini P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Komoto H., Okasaki Y., Muramatsu M. and Hayashizaki Y.				
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to identify novel genes for rapid discovery of new genes				
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)				
MEDLINE	20459374				
PUBMED	2049374				
REFERENCE	1 1042159				
AUTHORS	Shibata K., Itoh M., Aizawa K., Nagakura S., Saeki N., Caminici P., Komoto H., Akiyama J., Mihi K., Kitamura T., Tashiro H., Itoh M., Sumi M., Ishii Y., Nakamura S., Hazama N., Mishine T., Harada A., Yamamoto K., Matsumoto H., Sakaguchi S., Ikegami T., Washiwagi K., Yoneda S., Ishikawa K., Ogasawara K., Tanaka M., Takemura J., Okasaki Y., Muramatsu M., Inoue Y., Kita A. and Hayashizaki Y.				
TITLE	RKEN integrated sequence analysis (RISA) system -384-format				
JOURNAL	Nucleic Acids Res. 19 (11), 1757-1771 (2000)				
MEDLINE	20530911				
PUBMED	11076861				
REFERENCE	4				
AUTHORS	Arai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Aizawa K., Izawa M., Nishi K., Miyasawa K., Kondou J.Y., Fukuda S., Saito T., Ohazaki M., Gajbori T., Bono H., Kanekawa T., Saito R., Adachi K., Matsuda H., Bernheimer M., Banlov S., Casavant T., Knehl P., Lewis S., Matsui T., Nakatsuki C., King B., Kochiwa H., Quackenbush J., Schmitt L.M., Staubli F., Suzuki K., Tomita M., Wagner I., Washio T., Sakai K., Okido T., Furuno M., Aono H., Maldarelli R., Barth G., Blake D., Boffelli D., Bojunga N., Choudhury S., Fleischer C., Fujita M., Gariboldi M., Gutierrez-Castell D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Melina J., Mazzarelli J., Mombauris P.; Nordone P., Satoh K., Schombach C., Seya T., Shimizu S., Sakaki H., Sato K., Schombach C., Seya T., Shimizu S., Sakaki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Waltinger N., W				


```

- Web : www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
FEATURES
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BASE COUNT      203 a 154 c 331 g 203 t 10 others
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Query Match      17.1%; Score 40.8; DB 29; Length 941;
Best Local Similarity 56.1%; Prd. No. 1.2; Mismatches 5; Gaps 1;
Matches 108; Conservative 5; Mismatches 92; Indels 5; Gaps 1;
Qy 4 AGACACGTCGACATGATGCTGCTGACACCTGAGAGACTGACATCCCTGTCAC 63
Db 868 ATGTCGCGGACGAGGATGATGACGATGCTGCTGACACCTGAGAGACTGACATCCCTGTCAC 809
Qy 64 AATGTCATGTCGACGACGAGGAGGCGCCCAAGGCGCCCATCGCTTCTCTGATCATCAT 123
Db 808 ATGTCGCGGACGAGGATGATGACGATGCTGCTGACACCTGAGAGACTGACATCCCTGTCAC 809
Qy 124 TGTCTCTGATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 183
Db 808 ATGTCGCGGACGAGGATGATGACGATGCTGCTGACACCTGAGAGACTGACATCCCTGTCAC 809
Qy 751 --ATTCCTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 694
Db 184 CTATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 213
Qy 693 ATTCCTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 664
Db 693 ATTCCTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 664

RESULT 10
CONS2UEW      944 bp      DNA      linear      GSS 01-SEP-2000
Tetraodon nigroviridis genome survey sequence T7 end of clone
167023 of library G from Tetraodon nigroviridis, genomic survey
sequence.
ACCESSION     AL214370.1 GI:7871189
VERSION       GSS; genome survey sequence.
KEYWORDS      Tetraodon nigroviridis
SOURCE        Eukaryotic Genomes
ORGANISM      Tetraodon nigroviridis
MIMMALS; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorphi; Acanthopterygii; Percormorpha; Tetraodontiformes;
Tetraodontidae; Tetraodontidae; Tetraodon.
REFERENCE
AUTHORS       Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernet,A., Fianes,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
TITLE         The compact genome of the Tetraodon lineatus, a
freshwater pufferfish Tetraodon nigroviridis
JOURNAL       Genome Res. 10 (7), 939-949 (2000)
MEDLINE       20359837
PMID          10854340
KEYWORDS      3 (bases 1 to 844)
AUTHORS       Genoscope.
TITLE         Direct Submission

```

```

JOURNAL        Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 931 91060 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
COMMENT        This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
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        /map="Tetraodon"
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Best Local Similarity 56.1%; Prd. No. 1.2; Mismatches 0; Gaps 0;
Matches 60; Conservative 7; Mismatches 7; Indels 0; Gaps 0;
Qy 105 CTTCCTCTGTCGACATGCTGCTGACACCTGAGAGACTGACATCCCTGTCAC 164
Db 661 CATCTTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 602
Qy 165 ACCTTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 211
Db 601 ATCTCTCTGTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 555

RESULT 11
BH308136      611 bp      DNA      linear      GSS 03-DEC-2001
CH230-193A19-TJ CHORI-230 Segment 1 Rattus norvegicus genomic clone
BH308136.1 GI:17233605
ACCESSION     BH308136.1 GI:17233605
VERSION       GSS.
KEYWORDS      Rattus norvegicus (Norway rat)
SOURCE        Eukaryotic Genomes
ORGANISM      Rattus norvegicus
MIMMALS; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
AUTHORS       Zhao,S., Shetty,J., Shatman,S., Tsagaye,G., Geer,K., Shvartsbeyn,
A., Gebregorjisi,E., Overton,L., Russell,D., Chen,D., Riggs,F., de
Jong,P. and Fraser,C.M.
TITLE         Rat Rattus norvegicus genomic clone BH308136.1
JOURNAL       Unpublished Sequences from Library CHORI-230 Ecoli segment
COMMENT        Other GSSs: CH230-193A19-TV
Contact: Shaying Zhao
Department of Eukaryotic Genomes
The University of Maryland System
9712 Medical Center Dr., Rockville, MD 20850, USA
Fax: 301 838 0208
Tel: 301 838 0200
E-mail: zhao@genoscope.cns.fr
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Piet de Jong (pjejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(www.bacpac.com) or from the University of Maryland System
(www.genoscope.cns.fr).
Page: 193 row: A column: 19
Seq primer: SP6
Seq direction: 5' to 3'
Class: BACPAC
Location/Qualifiers
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    /mol_type="genomic DNA"
    /db_xref="taxon:10116"
    /map="BH308136"

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[illegible]

[illegible]

Mon Dec 8 11:25:46 2003

Qy 167 CTTTACCTCTGATC 182

Db 161 TCTACATATTATC 176

Search completed: December 5, 2003, 23:17:03
Job time : 100.088 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 5, 2003, 23:22:39 ; Search time 4840 Seconds
(without alignments)
10658.475 Million cell updates/sec

Title: US-09-936-680-4

Perfect score: 1261
Sequence: 1 cctccctccagtcgagc.....tcgccagactgagagccg 1261

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 2888711 seqs, 2045481396 residues

Word size : 10

Total number of hits satisfying chosen parameters: 2382734

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

GenBank:

1: gb.bcg*

2: gb.bcg*

3: gb.in*

4: gb.en*

5: gb.pat*

6: gb.pat*

7: gb.pat*

8: gb.pl*

9: gb.pl*

10: gb.pl*

11: gb.sgs*

12: gb.sv*

13: gb.vin*

14: gb.vin*

15: en.ba*

16: en.fun*

17: en.fun*

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22: en.fun*

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28: en.fun*

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30: en.fun*

31: en.fun*

32: en.fun*

33: en.fun*

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35: en.fun*

36: en.fun*

37: en.fun*

38: en.fun*

39: en.fun*

40: en.fun*

41: en.fun*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1261	100.0	1261	AX039100	Sequence
2	1174	87.5	1052	HS081153	Sequence
3	1104	87.5	4052	HS081153	Sequence
4	860	68.2	5206	AB032984	AB032984 Homo sapi
5	428	33.9	12347	AP000682	AP000682 Homo sapi
6	428	33.9	12347	AP000682	AP000682 Homo sapi
7	428	33.9	14980	AC021981	AC021981 Homo sapi
8	428	33.9	172546	AC024604	AC024604 Homo sapi
9	428	33.9	178159	AP002765	AP002765 Homo sapi
10	428	33.9	178159	AP002765	AP002765 Homo sapi
11	328	25.7	471	BD059018	BD059018 Secreted
12	262	20.8	178431	AP002749	AP002749 Homo sapi
13	226	17.9	172546	AC024604	AC024604 Homo sapi
14	220	17.4	142396	AB032984	AB032984 Homo sapi
15	218	17.4	142396	AB032984	AB032984 Homo sapi
16	218	17.4	14980	AC021981	AC021981 Homo sapi
17	216	17.1	178431	AP002749	AP002749 Homo sapi
18	143	11.3	66980	AC013796	AC013796 Homo sapi
19	138	11.3	66980	AC013796	AC013796 Homo sapi
20	38	3.0	645	AX048004	AX048004 Sequence
21	38	3.0	2220	AX039099	AX039099 Sequence
22	38	3.0	2220	AX039099	AX039099 Sequence
23	38	3.0	2220	AX039099	AX039099 Sequence
24	38	3.0	3177	AX019893	AX019893 Rattus no
25	38	3.0	3108	AX047984	AX047984 Sequence
26	29	2.3	670	AX045038	AX045038 Mus muscu
27	29	2.3	14264	AC132523	AC132523 Rattus no
28	29	2.3	14264	AC132523	AC132523 Rattus no
29	24	1.9	158801	AC079118	AC079118 Homo sapi
30	24	1.8	257	AX009586	AX009586 Bosphiliu
31	23	1.8	109446	AL645845	AL645845 House DNA
32	23	1.8	109446	AL645845	AL645845 House DNA
33	23	1.8	196383	AC113159	AC113159 Rattus no
34	23	1.8	198862	AC005528	AC005528 Mus muscu
35	23	1.8	24939	AC127850	AC127850 Rattus no
36	23	1.8	24939	AC127850	AC127850 Rattus no
37	23	1.8	271454	AC112098	AC112098 Rattus no
38	22	1.7	518	AF102248	AF102248 Obocollu
39	22	1.7	2322	AC135108	AC135108 Mus muscu
40	22	1.7	165095	BX537251	BX537251 Danio rer
41	22	1.7	165095	BX537251	BX537251 Danio rer
42	22	1.7	169757	AL627256	AL627256 Zebrafish
43	22	1.7	175930	BX089532	BX089532 Danio rer
44	22	1.7	175930	BX089532	BX089532 Danio rer
45	22	1.7	198896	AC114645	AC114645 Mus muscu

ALIGNMENTS

RESULT 1	AX039100	1261 bp	DNA	linear	PAF 18-NOV-2000
AX039100	Sequence 4 from Patent WO0063367.				
DEFINITION	Sequence 4 from Patent WO0063367.				
ACCESSION	AX039100				
VERSION	AX039100.1				
ORGANISM	Homo sapiens (human)				
SOURCE	Homo sapiens				
REFERENCE	Rikhyapota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	Cox,P., Dixon,A., Jackson,A. and Morgan,K.				
TITLE	A novel family of beta sub-unit proteins from a voltage-gated sodi				
	um channel, nucleic acids encoding them and therapeutic of				

Pred. No. is the number of results predicted by chance to have a

[illegible]

JOURNAL
COMMENT

Submitted (21-JUN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Jul 19, 2000 this sequence version replaced gl.6731265.
 All repeats were identified using RepeatMasker:
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Project name: 1315

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence submissions@genome.wi.mit.edu

----- Project Information

Center Project name: 1315

Center Project name: 1315

----- Summary Statistics

Sequencing vector: M13; M77815; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Read length: 800 bp
 Consensus quality: 13517 bases at least Q40
 Consensus quality: 141872 bases at least Q40
 Consensus quality: 144404 bases at least Q20
 Inset size: 147000; sum-of-coverage
 Quality coverage: 4.2 in Q20 bases; agatose-fp
 Quality coverage: 3.5 in Q20 bases; sum-of-coverage

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 29 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * dashes. The contigs are ordered by their accession number.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

* 1442 1441: contig of 1441 bp in length
 * 1442 1541: gap of 100 bp
 * 1542 2883: contig of 1342 bp in length
 * 2884 2983: gap of 100 bp
 * 2984 4256: contig of 1272 bp in length
 * 4256 4750: contig of 494 bp in length
 * 4750 6112: contig of 1363 bp in length
 * 6113 6212: gap of 100 bp
 * 6212 7113: contig of 901 bp in length
 * 7113 7514: contig of 401 bp in length
 * 7514 9051: contig of 1537 bp in length
 * 9051 9150: gap of 100 bp
 * 9151 10944: contig of 1794 bp in length
 * 10944 11045: contig of 100 bp
 * 11045 12031: contig of 2153 bp in length
 * 12031 13204: contig of 100 bp
 * 13204 16118: contig of 2815 bp in length
 * 16118 16713: gap of 595 bp in length
 * 16713 18774: contig of 2061 bp in length
 * 18774 18774: gap of 100 bp
 * 18774 21281: contig of 2407 bp in length
 * 21281 22300: gap of 100 bp
 * 22300 23301: contig of 1001 bp in length
 * 23301 26526: contig of 3226 bp in length
 * 26526 26526: gap of 100 bp
 * 26527 29756: contig of 3129 bp in length
 * 29756 34738: contig of 4983 bp in length
 * 34738 34738: gap of 100 bp
 * 34739 39495: contig of 5045 bp in length
 * 39495 43670: contig of 4175 bp in length
 * 43670 43769: gap of 100 bp
 * 43770 45578: contig of 6179 bp in length
 * 45578 50049: contig of 5310 bp in length
 * 50049 55579: gap of 100 bp
 * 55579 60959: contig of 5281 bp in length

* 60960 61059: gap of 100 bp
 * 61060 66394: contig of 5335 bp in length
 * 66395 66395: gap of 100 bp
 * 66395 72947: contig of 6453 bp in length
 * 72947 73048: gap of 100 bp
 * 73048 80875: contig of 6827 bp in length
 * 80875 80875: gap of 100 bp
 * 80875 87847: contig of 6873 bp in length
 * 87848 87848: gap of 100 bp
 * 87849 97379: gap of 100 bp
 * 97380 97379: gap of 100 bp
 * 97380 106037: contig of 8658 bp in length
 * 106038 106137: gap of 100 bp
 * 106138 114207: contig of 7069 bp in length
 * 114208 114208: contig of 100 bp
 * 114209 123830: contig of 15524 bp in length
 * 123831 123931: gap of 100 bp
 * 123931 124980: contig of 19870 bp in length.
 * 124980 124980: contig of 19870 bp in length.

----- RepeatMasker

organism="Homo sapiens"

mol_type="genomic DNA"

seq_id="us09-936-680-4"

chromosome="11"

map="11"

clone="RP11-11C15"

clone_lib="RP11-11 Human Male BAC"

note="assembly_fragment"

note="assembly_fragment"

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and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
 1-15-1 Kitasato, Saginawa, Kanagawa 228-8555, Japan
 (E-mail: hataori@gsc.riken.go.jp, URL: http://hsp.gsc.riken.go.jp/
 Tel: 81-42-778-9923, Fax: 81-42-778-9934)

----- Center: RIKEN Genomic Sciences Center (GSC)

Center code: RIKEN

Web site: http://hsp.gsc.riken.go.jp/

Contact: hataori@gsc.riken.go.jp

----- Center: Project Information

Center project name: HumDrafc11

Center clone name: RP1-158721

----- Sequencing Summary Statistics

Chemistry: Dye-terminator

Assembly: Phrap; version 0.990329

Consensus quality: 15592 bases at least Q40

Consensus quality: 170239 bases at least Q30

Insert size: 174431; sum-of-coverage

Quality coverage: 4.20x in Q20 bases; sum-of-coverage

NOTE: This is a 'working draft' sequence. It currently consists of

41 contigs. The true order of the pieces is not known and their

order in this sequence record is arbitrary. Gaps between the

contigs are represented as runs N, but the exact sizes of the gaps

as soon as it is available and the accession number will be

preserved.

1

13111

13112

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13170

arbitrary. Gaps between the contigs are represented as
 runs of N, but the exact sizes of the gaps are unknown.
 This record will be updated with the finished sequence
 as soon as it is available and the accession number will
 be preserved.

13012: contig of 13012 bp in length
 13013: gap of 100 bp
 13113: contig of 11565 bp in length
 13114: gap of 100 bp
 13115: contig of 100 bp
 13116: gap of 100 bp
 13117: gap of 100 bp
 13118: contig of 8456 bp in length
 13119: gap of 100 bp
 13120: contig of 680 bp in length
 13121: gap of 100 bp
 13122: contig of 7159 bp in length
 13123: gap of 100 bp
 13124: contig of 6787 bp in length
 13125: gap of 100 bp
 13126: contig of 6287 bp in length
 13127: gap of 100 bp
 13128: contig of 5089 bp in length
 13129: gap of 100 bp
 13130: contig of 7239 bp in length
 13131: gap of 100 bp
 13132: contig of 6811 bp in length
 13133: gap of 100 bp
 13134: contig of 6811 bp in length
 13135: gap of 100 bp
 13136: contig of 6811 bp in length
 13137: gap of 100 bp
 13138: contig of 6811 bp in length
 13139: gap of 100 bp
 13140: contig of 6811 bp in length
 13141: gap of 100 bp
 13142: contig of 6811 bp in length
 13143: gap of 100 bp
 13144: contig of 6811 bp in length
 13145: gap of 100 bp
 13146: contig of 6811 bp in length
 13147: gap of 100 bp
 13148: contig of 6811 bp in length
 13149: gap of 100 bp
 13150: contig of 6811 bp in length
 13151: gap of 100 bp
 13152: contig of 6811 bp in length
 13153: gap of 100 bp
 13154: contig of 6811 bp in length
 13155: gap of 100 bp
 13156: contig of 6811 bp in length
 13157: gap of 100 bp
 13158: contig of 6811 bp in length
 13159: gap of 100 bp
 13160: contig of 6811 bp in length
 13161: gap of 100 bp
 13162: contig of 6811 bp in length
 13163: gap of 100 bp
 13164: contig of 6811 bp in length
 13165: gap of 100 bp
 13166: contig of 6811 bp in length
 13167: gap of 100 bp
 13168: contig of 6811 bp in length
 13169: gap of 100 bp
 13170: contig of 6811 bp in length

NOTE: This is a 'working draft' sequence. It currently
 consists of 41 contigs. The true order of the pieces
 is not known and their order in this sequence record is

```

* 167137 169169: contig of 2033 bp in length
* 167138 171053: gap of 1763 bp in length
* 169270 171053: gap of 100 bp
* 171053 171153: gap of 100 bp
* 171153 172933: contig of 1781 bp in length
* 172933 173034: gap of 100 bp
* 173034 174180: gap of 1147 bp in length
* 174180 174280: gap of 100 bp
* 174280 175729: contig of 1449 bp in length
* 175729 175805: gap of 76 bp in length
* 175805 175930: gap of 106 bp in length
* 175930 177005: gap of 100 bp
* 177005 178431: contig of 1436 bp in length.
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/map="11q24"
/clone="RP11-150J21"
1. .13013 assembly_fragment"
13113. 24677
/misc_feature
24778. 24640 fly_fragment"
24781. 431396
/misc_feature
24781. 431396 fly_fragment"
/misc_feature
43297. 50126 fly_fragment"
/misc_feature
50227. 57725
/misc_feature
57826. 64612
Query Match 20.8%; Score 362; DB 2; Length 178431;
Best Local Similarity 99.7%; Pred. No. 3e-138;
Matches 382; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 49 GGGCGGAGTGAAGTTCAGAGTTCGGGGTGGCGGGAGGAGCACTGCTGGTGGTGA 108
DB 111412 GGGCGGAGTGAAGTTCAGAGTTCGGGGTGGCGGGAGGAGCACTGCTGGTGGTGA 111411
QY 109 GCGCGCGGCGAGCGGGCGGAGGCGGTGATCGGCTCTCCGACTGGAGGAGTCCAGT 168
DB 111472 GCGCGCGGCGAGCGGGCGGAGGCGGTGATCGGCTCTCCGACTGGAGGAGTCCAGT 111531
QY 169 GGGGCTGGCTTAGGG-CTCAAGACCCCGACCGGCTCCAAAGCTCCAGGCGCTCCAG 227
DB 111532 GGGGCTGGCTTAGGG-CTCAAGACCCCGACCGGCTCCAAAGCTCCAGGCGCTCCAG 111591
QY 228 GCAAGCGGCTGTCGAGCTCTCTGCTGGTTCAGAAAGTGGTCCCTCGGAGGAGTTCGCCA 287
DB 111592 GCAAGCGGCTGTCGAGCTCTCTGCTGGTTCAGAAAGTGGTCCCTCGGAGGAGTTCGCCA 111651
QY 288 AAGGCTGTCCTGAGGAATTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 347
DB 111652 AAGGCTGTCCTGAGGAATTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 111711
QY 348 TACGCTCTGAGGCGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 407
DB 111712 TACGCTCTGAGGCGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 111771
QY 408 TCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 430
DB 111772 TCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 111794

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RESULT 13
 AC024604/c
 LOCUS
 DEFINITION
 Homo sapiens chromosome 17:3546 bp DNA linear HTG 30-AUG-2001
 DRAP SEQUENCE, 22 uncloned pieces.

```

AC024604.3 GL189426
HTG: HTGS PHASE1; HTGS_DRAFT; HTGS_CANCELLED.
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Mammalia: Eutheria: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1. (bases 1 to 172546)
Smith, P.R. Genomics Corporation Sequencing Center: Human Genome
Sequence Data
Unpublished
2. (bases 1 to 172546)
Direct Submission
Submitted (01-MAR-2000) Genome Therapeutics Corporation, 100 Beaver
Street, Waltham, MA 02453, USA
On Jun 9, 2000, this record version replaced GI:7549605.
Genome Center
Center: Genomics Corporation
Center code: GTC /www.genomacorp.com/
Center name: Genomics Corporation
Center address: 100 Beaver Street, Waltham, MA 02453, USA
Center phone: 781-890-1300
Center fax: 781-890-1301
Center email: gtc@genomacorp.com
Center web: www.genomacorp.com
Center project name: hg202
Sequencing Summary Statistics
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly: Phrap; version 990315
Consensus quality: 152033 bases at least Q40
Consensus quality: 152033 bases at least Q30
Consensus quality: 165256 bases at least Q20
Insert size: 170446; sum-of-Contigs
Quality coverage: 4.3x in Q20 bases; sum-of-Contigs
* NOTE: This is a 'working draft' sequence. It currently
* consists of 22 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* therefore arbitrary. The gaps between the contigs are
* numbered N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1340 1439: gap of 1339 bp in length
* 1440 2789: contig of 1350 bp in length
* 2789 2890: gap of 100 bp in length
* 2890 4562: gap of 1672 bp in length
* 4562 4663: gap of unknown length
* 4663 6344: contig of 1682 bp in length
* 6344 9341: gap of unknown length
* 9341 9342: gap of unknown length
* 9342 9322: gap of unknown length
* 9322 11597: contig of 2676 bp in length
* 11597 12897: gap of unknown length
* 12897 14868: gap of unknown length
* 14868 19519: contig of 4952 bp in length
* 19519 20019: gap of unknown length
* 20019 39920: gap of unknown length
* 39920 24126: gap of unknown length
* 24126 24226: gap of unknown length
* 24226 29444: contig of 5219 bp in length
* 29444 29445: gap of unknown length
* 29445 34668: gap of unknown length
* 34668 39414: contig of 4746 bp in length
* 39414 39514: gap of unknown length
* 39514 45981: contig of 6467 bp in length
* 45981 45982: contig of unknown length
* 45982 50997: contig of 5012 bp in length
* 50997 50998: gap of unknown length
* 50998 59143: contig of 8046 bp in length
* 59143 59144: gap of unknown length

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Search completed: December 6, 2003, 00:54:02
Job time : 4845 secs

DB 595 TTCTCTATTATTCAGTATTCAGATATGTCACACGAGAGTGTGAGAGCCCC 642

RESULT 5
AL534136 1201 bp mRNA linear EST 12-MAY-2003
DEFINITION CSDDP005Y102 5-PRIME, mRNA sequence.
ACCESSION AL534136
KEYWORDS EST, 5'UTR, 3'UTR
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1. (Bases 1 to 1201)
AUTHORS Li, M. B., Gruber, C. J., Jessee, J., and Polyssey, D.
JOURNAL The Journal of Molecular Biology
COMMENT On Feb 13, 2001 this sequence version replaced gi:12797629.
Contact: Genoscope
Genoscope, Centre National de Sequencage
Bâtiment 1006 RIVE, France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by life technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6147.f For
more information on this cluster, see
http://www.genoscope.cns.fr/
seq-bin/cluster.cgi?seq=CSDDP005Y102&cluster=6147.f. Contact :
Peng Jiang Email: jiangpeng@tech.cmu.edu
Genoscope, Centre National de Sequencage
Paradey Avenue Genoscope sequence ID : CSDDP005Y102P1.
FEATURES
source
1..1201
/locus="Homo sapiens"
/db_xref="taxon:9606"
/clone="CSDDP005Y102"
/db_xref="taxon:9606"
/dev_stage="fetal"
/clone_lib="Homo sapiens FETAL BRAIN"
/notes="Organ: brain; Vector: pCMVSPORT.6; 1st strand cDNA
library; 1st strand cDNA was digested with Not I and
enriched; double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."
BASE COUNT 221 a 331 c 402 g 214 t 33 Others
ORIGIN
Query Match 21.3%; Score 268; DB 91; Length 1201;
Best Local Similarity 99.54; Pred. No. 1.7e-68;
Matches 389; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 134 GCGTATCGGCTTCTGAGATCGGAGGTCGATGGTTCCTTGGGCGGAGAGCCC 193
DB 588 GAGTATCGGCTTCTGAGATCGGAGGTCGATGGTTCCTTGGGCGGAGAGCCC 647
QY 194 CCGGCTGCGTCAAGGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAG 253
DB 648 CCGGCTGCGTCAAGGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAG 707
QY 254 TCGAGAGTCCGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAG 313
DB 708 TCGAGAGTCCGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAG 767
QY 314 GGGGCGAGTCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAG 373
DB 768 GGGGCGAGTCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAG 826
QY 374 AGATGCTTCGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAG 433
DB 827 AGATGCTTCGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAG 886

QY 434 GTATTCGCTTCGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAG 493
DB 887 GTATTCGCTTCGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAG 946

QY 494 CATTGAGCTTCGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAG 522
DB 947 CATTGAGCTTCGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAG 975

RESULT 6
D44825 443 bp mRNA linear EST 20-FEB-1998
LOCUS HUMSUPY279 Human brain cDNA Homo sapiens cDNA Clone NF220-K, mRNA
DEFINITION D44825
ACCESSION D44825.1 GI:1572300
KEYWORDS EST, 5'UTR, 3'UTR
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1. (Bases 1 to 443)
AUTHORS Okuyama, Metaxa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Reptalia; Primates; Carnivora; Hominoidea; Hominidae; Homo.
JOURNAL The Journal of Molecular Biology
COMMENT Transcription of the human chromosome 4p16.3 consisting of 627
cDNA clones derived from a library of the Huntington's disease locus
region (11 kb) (1), 259-258 (1396)
97101646
8946164
Contact: Shinji Hadano
Genoscope, Centre National de Sequencage
Paradey Avenue Genoscope sequence ID : CSDDP005Y102P1.
Univ. of Tokai School of Med.
Bohseidai, Isehara, Kanagawa 259-1193, Japan
Tel: 81-463-91-5095
Fax: 81-463-91-5096
Email: shini@genoscope.cns.fr, shini@tokai.ac.jp.
FEATURES
source
1..443
/locus="Homo sapiens"
/db_xref="taxon:9606"
/clone="NF220-K"
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/dev_stage="fetal"
/clone_lib="Human brain cDNA"
BASE COUNT 111 a 136 c 82 g 120 t
ORIGIN
Query Match 13.1%; Score 165; DB 14; Length 443;
Best Local Similarity 99.54; Pred. No. 1.7e-68;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1044 AGGTGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAG 1103
DB 33 AGGTGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAG 92
QY 1104 GAGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1163
DB 93 GAGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 152
QY 1164 CATCTGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAG 1223
DB 153 CATCTGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAG 1289
QY 1224 CTGAGGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAG 212
DB 213 CTGAGGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAG 248

RESULT 7
BX280396 509 bp mRNA linear EST 04-MAR-2003
LOCUS BX280396 NIH_MGC_121 Homo sapiens cDNA Clone IMAG099F041282, 1;
DEFINITION

ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 (Date: 11/25/2003 to 6/16/2003)
 AUTHORS Bonaldo, M. P., G. and Soares M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene
 discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 PUBMED 8839548
 COMMENT Contact: Chin, H
 National Institute of Mental Health
 101 Bethesda Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
 20892-9643, USA
 Tel: 301 443 1706
 Fax: 301 443 9890
 Email: hchinn@mail.nih.gov
 CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research
 Center for Genome Sciences and Policy
 Seq primer: M13 REVERSE.

FEATURES

source
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 /organism="Mus musculus"
 /mol_type="mRNA"
 /seq_id="5781"
 /strain="C57BL/6J"
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 /locus_tag="Mmus23183gq-04-0-UT"
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 /clone_lib="NIH-BMAP_M_S4"
 /note="Vector: pVT730-Pac (Pharmacia) with a modified
 BamHI site. The NIH-BMAP_M_S4 library is a modified
 NIH-BMAP_M_S4 library is a subtracted library of a series,
 ultimately derived from a mixture of individually tagged,
 normalized libraries from ten regions of the mouse brain
 (cortex, amygdala, basal ganglia, pineal gland, hippocampus,
 hypothalamus, and thalamus) which were subtracted
 (hippocampus) after a series of subtractions to reduce the
 representation of cDNAs from which ESTs had already been
 generated. The following serially subtracted libraries
 were subtracted from the NIH-BMAP_M_S4 library:
 NIH-BMAP_M_S3.3, NIH-BMAP_M_S3.2, NIH-BMAP_M_S3.1,
 NIH-BMAP_M_S2, NIH-BMAP_M_S1. The subtracted library
 (NIH-BMAP_M_S4) was constructed as follows: PCR amplified
 cDNAs from the NIH-BMAP_M_S4 library were digested with
 NIH-BMAP_M_S3.1 clones from which 3' ESTs had been
 used as a driver in a hybridization with a pool of
 the NIH-BMAP_M_S3.3, NIH-BMAP_M_S3.2, and NIH-BMAP_M_S3.1
 clones. The resulting single-stranded cDNA library
 remaining single-stranded cDNA library was
 converted to double-stranded circles and electroporated
 into the NIH-BMAP_M_S4 library. The resulting
 NIH-BMAP_M_S4 library (Life Technologies) to generate the
 NIH-BMAP_M_S4 library. The NIH-BMAP_M_S4 library was
 described (Bonaldo, Lennon and Soares, Genome Research
 6:791-806, 1996)."
 BASE COUNT 158 a 154 c 169 g 135 t
 ORIGIN

Query Match 2.3%; Score 29; DB 12; Length 636;

Best Local Similarity 100.0%; Pred. No. 0.01;

Mismatches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 610 ATATGGCCACGAGGTGGAGAGCCCTT 638

DB 241 ATATGGCCACGAGGTGGAGAGCCCTT 269

Search completed: December 6, 2003, 01:44:39

Job time : 3032 secs

Db 61 GTCTGCTTCCTCTGTGTGGAGTGCCCTCGAGAC 98
|||||

RESULT 4

US-09-997-579-3

Sequence 22, Application US/0997579

Publication No. US2002013203A1

GENERAL INFORMATION:

APPLICANT: Cambridge University Technical Services

TITLE OF INVENTION: A family of beta sub-unit proteins from a voltage gated sodium channel

TITLE OF INVENTION: nucleic acids encoding them and therapeutic or diagnostic uses thereof

FILE REFERENCE: 674558-2001

CURRENT APPLICATION NUMBER: US/09/997,579

PRIOR APPLICATION NUMBER: PCT/EP00/01783

PRIOR FILING DATE: 2000-02-24

PRIOR FILING DATE: 2000-02-24

NUMBER OF SEQ ID NOS: 47

SOFTWARE: PatentIn version 3.1

SEQ ID NO 3

ORGANISM: Rattus sp.

TYPE: DNA

US-09-997-579-3

Query Match Best Local Similarity 100.0%; Pred. No. 7; Length 2220;

Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Yy 436 GTCTGCTTCCTCTGTGTGGAGTGCCCTCGAGAC 473

Db 423 GTCTGCTTCCTCTGTGTGGAGTGCCCTCGAGAC 460

RESULT 5

US-10-029-191-22

Sequence 22, Application US/10029191

Publication No. US20020160453A1

GENERAL INFORMATION:

APPLICANT: CURTIS, Rory A.J.

TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT

TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT

FILE REFERENCE: 10029191

CURRENT APPLICATION NUMBER: US/10/029,191

PRIOR APPLICATION NUMBER: 09/569,978

PRIOR FILING DATE: 2001-12-20

PRIOR FILING DATE: 1999-05-14

NUMBER OF SEQ ID NOS: 23

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2632

ORGANISM: Rattus sp.

TYPE: DNA

US-10-029-191-22

Query Match Best Local Similarity 100.0%; Pred. No. 7; Length 2632;

Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Yy 436 GTCTGCTTCCTCTGTGTGGAGTGCCCTCGAGAC 473

Db 138 GTCTGCTTCCTCTGTGTGGAGTGCCCTCGAGAC 175

RESULT 6

US-10-029-191-1

Sequence 1, Application US/10029191

Publication No. US20020160453A1

GENERAL INFORMATION:

APPLICANT: CURTIS, Rory A.J.

TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT

TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT

FILE REFERENCE: 10029191

CURRENT APPLICATION NUMBER: US/10/029,191

PRIOR APPLICATION NUMBER: 09/569,978

PRIOR FILING DATE: 2001-12-20

PRIOR FILING DATE: 1999-05-14

NUMBER OF SEQ ID NOS: 23

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2632

ORGANISM: Rattus sp.

TYPE: DNA

US-10-029-191-22

Query Match Best Local Similarity 100.0%; Pred. No. 7; Length 2632;

Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Yy 436 GTCTGCTTCCTCTGTGTGGAGTGCCCTCGAGAC 473

Db 138 GTCTGCTTCCTCTGTGTGGAGTGCCCTCGAGAC 175

GENERAL INFORMATION:

APPLICANT: CURTIS, Rory A.J.

TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT

TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT

FILE REFERENCE: 210147, 00XX/501

CURRENT APPLICATION NUMBER: US/10/029,191

PRIOR APPLICATION NUMBER: 2001-12-20

PRIOR FILING DATE: 2000-06-12

PRIOR FILING DATE: 2000-06-12

PRIOR FILING DATE: 1999-05-14

NUMBER OF SEQ ID NOS: 23

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1

LENGTH: 3108

TYPE: DNA

US-10-029-191-1

Query Match Best Local Similarity 100.0%; Pred. No. 6; Length 3108;

Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Yy 436 GTCTGCTTCCTCTGTGTGGAGTGCCCTCGAGAC 473

Db 138 GTCTGCTTCCTCTGTGTGGAGTGCCCTCGAGAC 175

RESULT 7

US-09-1293

Sequence 1233, Application US/09764891

Publication No. US2003007808A1

GENERAL INFORMATION:

APPLICANT: ROSEN, et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PC006

CURRENT APPLICATION NUMBER: US/09/764,891

PRIOR APPLICATION NUMBER: 2001-01-17

PRIOR FILING DATE: 2001-01-17

NUMBER OF SEQ ID NOS: 10231

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1293

ORGANISM: Homo sapiens

TYPE: DNA

US-09-1293

Query Match Best Local Similarity 100.0%; Pred. No. 6; Length 1293;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Yy 1227 GCACCATAGACTCTCCGAGACTCGAGAGCC 1259

Db 2 CCNCATAGACTCTCCGAGACTCGAGAGCC 34

RESULT 8

100

Query Match 1.6%; Score 20; DB 14; Length 2884;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 20; Conservative 0; Mismatches 0; Indels

QY 500 AGCTGGCTGCATCTCTCTCC 519
DB 347 AGCTGGCTGCATCTCTCTCC 328

RESULT 15

US 09-936-679-679/G
; SEQ-Id: 679; Application US/09864761

; Patent No. US20020048763A1

; GENERAL INFORMATION:

; APPLICANT: Penn, Sharon G.

; INVENTOR: Harel, David K.

; APPLICANT: Harel, David K.

; APPLICANT: Chen, Rensheng

; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: GENE EXPRESSION ANALYSIS BY MICROARRAY

; CURRENT APPLICATION NUMBER: US/09/864,761

; CURRENT FILING DATE: 2001-05-23

; PRIOR APPLICATION NUMBER: US 60/180,312

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: US 09/632,366

; PRIOR FILING DATE: 2000-06-08

; PRIOR APPLICATION NUMBER: GB 24263, 6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: US001/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00662

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00661

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00670

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: US 60/234,687

; PRIOR FILING DATE: 2000-06-30

; PRIOR APPLICATION NUMBER: US 09/608,408

; PRIOR FILING DATE: 2000-06-30

; PRIOR APPLICATION NUMBER: US 09/774,203

; PRIOR FILING DATE: 2000-06-30

; NUMBER OF SEQ ID NOS: 117

; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1

; SEQ ID NO 679

; LENGTH: 187

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: MAP TO AC007076.2

; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 13

; OTHER INFORMATION: EXPRESSED IN KIDNEY, SIGNAL = 18

; OTHER INFORMATION: EXPRESSED IN HELI00, SIGNAL = 11

; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 14

; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 15

; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 9.8

; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 12

; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 16

; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 12
US-09-964-761-679

Query Match 1.5%; Score 19; DB 9; Length 471;
Local Similarity 100.0%; Pred. No. 15;
Matches 19; Conservative 0; Mismatches 0; Gaps 0;

QY 521 TGAAGAGAGAGAGAGGTGGG 539

DB 209 TGAAGAGAGAGAGAGGTGGG 191

Search completed: December 6, 2003, 01:54:59
Job time : 497 secs

Best Local Similarity 8.4%; pred. No. 0.023; 77; Indels 0; Gaps 0;
Matches 109; Conservative 109; Mismatches

QY 20 GAGTGGCTGAACACCTGAGGAGCTGACGATGTCAGCATGTCATGCGATCA 79
DB 1035 GAGTGGCTGAACACCTGAGGAGCTGACGATGTCAGCATGTCATGCGATCA 1094
QY 80 GAGTGGCTGAACACCTGAGGAGCTGACGATGTCAGCATGTCATGCGATCA 139
DB 1035 GAGTGGCTGAACACCTGAGGAGCTGACGATGTCAGCATGTCATGCGATCA 1154
QY 1095 YY 1154
DB 140 TATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1154
QY 140 TATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1154
DB 1155 YY 1214
QY 200 TCTACGACCAAGATGCTCC 222
DB 1215 YYYYYYYYYYYYYYYYYYYYYY 1237

RESULT 2
US-08-961-810-14/c
Patent No. 6165713
GENERAL INFORMATION:
APPLICANT: Liskey, Robert M.
INVENTOR: Liskey, Robert M.
APPLICANT: Branner, Sean M.
APPLICANT: Bollag, Roni J.
APPLICANT: Kolodner, Richard D.
TITLE OF INVENTION: MISMATCH REPAIR GENES
NUMBER OF SEQUENCES: 134
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kollisch, Hartwell, Dickinson, McCormack &
CITY: Portland
STATE: Oregon
COUNTRY: U.S.A.
ZIP: 97204
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 09/08/961,810
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 33,557
REFERENCE/DOCKET NUMBER: OHSU 306B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 295-6679
TELEFAX: (503) 295-6679
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 1237
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
Query Match
Best Local Similarity 14.3%; Score 34; DB 3; Length 526;
Matches 40; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 107 TCCCTTCATCATCATTCATTCCTGTTTATCCCATTCACCAACCATCTCC 156
DB 107 TCCCTTCATCATCATTCATTCCTGTTTATCCCATTCACCAACCATCTCC 156

RESULT 4
US-09-265-503B-14/c
Patent No. 633108
GENERAL INFORMATION:
APPLICANT: Liskey, Robert M.
INVENTOR: Liskey, Robert M.
APPLICANT: Branner, Sean M.
APPLICANT: Bollag, Roni J.
APPLICANT: Kolodner, Richard D.
TITLE OF INVENTION: MISMATCH REPAIR GENES
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kollisch, Hartwell, Dickinson, McCormack &
CITY: Portland
STATE: Oregon
COUNTRY: U.S.A.
ZIP: 97204
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 09/08/961,810
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 33,557
REFERENCE/DOCKET NUMBER: OHSU 306B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 295-6679
TELEFAX: (503) 295-6679
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 148
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
Query Match
Best Local Similarity 14.3%; Score 34; DB 3; Length 526;
Matches 40; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 107 TCCCTTCATCATCATTCATTCCTGTTTATCCCATTCACCAACCATCTCC 156
DB 107 TCCCTTCATCATCATTCATTCCTGTTTATCCCATTCACCAACCATCTCC 156

RESULT 4
US-09-265-503B-14/c
Patent No. 633108
GENERAL INFORMATION:
APPLICANT: Liskey, Robert M.
INVENTOR: Liskey, Robert M.
APPLICANT: Branner, Sean M.
APPLICANT: Bollag, Roni J.
APPLICANT: Kolodner, Richard D.
TITLE OF INVENTION: MISMATCH REPAIR GENES
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kollisch, Hartwell, Dickinson, McCormack &
CITY: Portland
STATE: Oregon
COUNTRY: U.S.A.
ZIP: 97204
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 09/08/961,810
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 33,557
REFERENCE/DOCKET NUMBER: OHSU 306B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 295-6679
TELEFAX: (503) 295-6679
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 148
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
Query Match
Best Local Similarity 14.3%; Score 34; DB 3; Length 526;
Matches 40; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 107 TCCCTTCATCATCATTCATTCCTGTTTATCCCATTCACCAACCATCTCC 156
DB 107 TCCCTTCATCATCATTCATTCCTGTTTATCCCATTCACCAACCATCTCC 156

DB 107 TCCCTTCATCATCATTCATTCCTGTTTATCCCATTCACCAACCATCTCC 58
RESULT 3
US-08-352-902D-14/c
Patent No. 619168
GENERAL INFORMATION:
APPLICANT: Liskey, Robert M.
INVENTOR: Liskey, Robert M.
APPLICANT: Branner, Sean M.
APPLICANT: Bollag, Roni J.
APPLICANT: Kolodner, Richard D.
TITLE OF INVENTION: MISMATCH REPAIR GENES
NUMBER OF SEQUENCES: 149
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kollisch, Hartwell, Dickinson, McCormack &
CITY: Portland
STATE: Oregon
COUNTRY: U.S.A.
ZIP: 97204
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 09/08/952,902D
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 33,557
REFERENCE/DOCKET NUMBER: OHSU 306B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 224-5655
TELEFAX: (503) 295-6679
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 149
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
Query Match
Best Local Similarity 14.3%; Score 34; DB 3; Length 526;
Matches 40; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 107 TCCCTTCATCATCATTCATTCCTGTTTATCCCATTCACCAACCATCTCC 156
DB 107 TCCCTTCATCATCATTCATTCCTGTTTATCCCATTCACCAACCATCTCC 156

RESULT 4
US-09-265-503B-14/c
Patent No. 633108
GENERAL INFORMATION:
APPLICANT: Liskey, Robert M.
INVENTOR: Liskey, Robert M.
APPLICANT: Branner, Sean M.
APPLICANT: Bollag, Roni J.
APPLICANT: Kolodner, Richard D.
TITLE OF INVENTION: MISMATCH REPAIR GENES
NUMBER OF SEQUENCES: 149
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kollisch, Hartwell, Dickinson, McCormack &
CITY: Portland
STATE: Oregon
COUNTRY: U.S.A.
ZIP: 97204
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 09/08/952,902D
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 33,557
REFERENCE/DOCKET NUMBER: OHSU 306B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 224-5655
TELEFAX: (503) 295-6679
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 149
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
Query Match
Best Local Similarity 14.3%; Score 34; DB 3; Length 526;
Matches 40; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 107 TCCCTTCATCATCATTCATTCCTGTTTATCCCATTCACCAACCATCTCC 156
DB 107 TCCCTTCATCATCATTCATTCCTGTTTATCCCATTCACCAACCATCTCC 156

RESULT 4
US-09-265-503B-14/c
Patent No. 633108
GENERAL INFORMATION:
APPLICANT: Liskey, Robert M.
INVENTOR: Liskey, Robert M.
APPLICANT: Branner, Sean M.
APPLICANT: Bollag, Roni J.
APPLICANT: Kolodner, Richard D.
TITLE OF INVENTION: MISMATCH REPAIR GENES
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kollisch, Hartwell, Dickinson, McCormack &
CITY: Portland
STATE: Oregon
COUNTRY: U.S.A.
ZIP: 97204
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 09/08/952,902D
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 33,557
REFERENCE/DOCKET NUMBER: OHSU 306B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 224-5655
TELEFAX: (503) 295-6679
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 148
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
Query Match
Best Local Similarity 14.3%; Score 34; DB 3; Length 526;
Matches 40; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 107 TCCCTTCATCATCATTCATTCCTGTTTATCCCATTCACCAACCATCTCC 156
DB 107 TCCCTTCATCATCATTCATTCCTGTTTATCCCATTCACCAACCATCTCC 156

RESULT 4
US-09-265-503B-14/c
Patent No. 633108
GENERAL INFORMATION:
APPLICANT: Liskey, Robert M.
INVENTOR: Liskey, Robert M.
APPLICANT: Branner, Sean M.
APPLICANT: Bollag, Roni J.
APPLICANT: Kolodner, Richard D.
TITLE OF INVENTION: MISMATCH REPAIR GENES
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kollisch, Hartwell, Dickinson, McCormack &
CITY: Portland
STATE: Oregon
COUNTRY: U.S.A.
ZIP: 97204
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 09/08/952,902D
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 33,557
REFERENCE/DOCKET NUMBER: OHSU 306B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 224-5655
TELEFAX: (503) 295-6679
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 148
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
Query Match
Best Local Similarity 14.3%; Score 34; DB 3; Length 526;
Matches 40; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 107 TCCCTTCATCATCATTCATTCCTGTTTATCCCATTCACCAACCATCTCC 156
DB 107 TCCCTTCATCATCATTCATTCCTGTTTATCCCATTCACCAACCATCTCC 156


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CLASSIFICATION: DATA
PRIOR APPLICATION DATE: US 60/029, 679
PUBLICATION NUMBER: 38 OCT-1996
FILING DATE: 30 OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/038, 056
FILING DATE: 09-OCT-1996
PUBLICATION NUMBER: 38 OCT-1996
APPLICATION NUMBER: US 60/025, 719
FILING DATE: 10-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Wilson Mack B. 37, 259
ADDRESS: 1000 N. 1st St. #100
CITY: Phoenix AZ 85004
TELEPHONE: 512/418-3000
REFERENCE/DOCKET NUMBER: ARCD-272
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
FAX: 512/418-3007
ELECTRONIC MAIL ADDRESS:
INFORMATION FOR SEQ ID NO: 126:
SEQUENCE CHARACTERISTICS:
LENGTH: 6254 base pairs
TYPE: nucleic acid
SOURCE: Human genome
TOPOLOGY: linear
FEATURE:
NAME/KEY: modified base
START: 1267-1473
OTHER INFORMATION: /docseq= "N = A or G or C or T"
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Sequence Similarity 7.2%; GC 48%
Matches 12; Conservative 17; Indels 0; Gaps 0
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1368 CRITICAL POINTS IDENTIFIED IN THE COMPARISON OF SEQUENCE 1425

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RESULT 10
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 1 SEQUENCE 9, APPLICATION US/08332766A
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 3 GENERAL INFORMATION:
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 5 APPLICANT: JEFFREYS, ALEC J.
 6 APPLICANT: JEFFREYS, ALEC J.
 7 APPLICANT INVENTOR: JEFFREYS, ALEC J.
 8 APPLICANT INVENTOR: JEFFREYS, ALEC J.
 9 SINGLE TANDEM REPEATS
 10 NUMBER OF SEQUENCES: 125
 11
 12 CORRESPONDENCE ADDRESS: 125
 13 JAMES H. COOPER AVE. & CHURMAN, L.L.P.
 14 STREET 1100 NEW YORK AVENUE, N.W.
 15 CITY: Washington
 16 STATE: D. C.
 17 COUNTRY: U.S.A.
 18 ZIP: 20005-3918
 19
 20 COMPUTER READABLE FORM:
 21
 22 MEDIUM TYPE: floppy disk
 23 OPERATING SYSTEM: PC-DOS/MS-DOS
 24 SOFTWARE: Patent Release #1.0, Version #1.25
 25
 26 COUNTRY OF ORIGIN: U.S.A.
 27 PUBLICATION NUMBER: US/08/332,766A
 28 FILING DATE: 01-NOV-1994
 29
 30 CLASSIFICATION: 435
 31 PRIORITY CLAIM: NO
 32 APPLICATION NUMBER: GB 9326052.9
 33
 34 FILING DATE: 21-DEC-1993
 35
 36 ATTORNEY/AGENT INFORMATION:
 37
 38 FIRM: JAMES H. COOPER AVE. & CHURMAN, L.L.P.
 39 REGISTRATION NUMBER: U.S. 25,323
 40
 41 REFERENCE/DOCKET NUMBER: 217211/M94/0434/GB
 42
 43 TELECOMMUNICATION INFORMATION:
 44
 45 TELEPHONE: 202-822-0600
 46 TELEFAX: 202-822-0344

GenCore version 5.1.6
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ON nucleic - nucleic search, using sw model

Run on: December 5, 2003, 23:19:13 ; Search time 441 seconds
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US-09-936-680-4

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Gapop 60.0 , Gapext 60.0

Searched: 2552756 seqs, 1349719017 residues

Word size : 10

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Minimum DB seq length: 0

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
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2	1104	87.5	4052	24 AAS93727	Human signal transduction domain
3	1004	86.3	1978	22 AAS98320	Human EST-derived
4	799	62.4	1045	22 AAK52345	Human polynucleotid
5	787	62.4	1045	22 AAK52345	DNA encoding novel
6	396	31.4	1195	23 AAS86764	DNA encoding novel
7	391	31.0	3531	23 AAS86695	EST Clone BM7. No
8	324	25.7	471	20 AAS6695	

9	218	17.2	631	23 AAS6762	DNA encoding novel
10	216	17.1	4625	23 AAL04971	Human reproductive
11	216	17.1	4625	23 AAL04971	Human testicular a
12	91	7.2	407	22 AAN07864	Human voltage-gate
13	71	5.9	509	22 AAS13385	Human polyomucleo
14	71	5.9	509	22 AAS13385	Human polyomucleo
15	38	3.0	645	22 AAS0601	Rat beta3 channel
16	38	3.0	2220	21 AAC67838	Rat beta3 subunit
17	38	3.0	2220	21 AAC67838	Human beta3 subun
18	33	2.6	3108	22 AAS0600	Rat sodium channel
19	33	2.6	574	22 AAL01292	Human reproductive
20	33	2.6	574	22 AAL01292	Human testicular a
21	28	2.2	465	22 AAS6750	Human beta3 subun
22	28	2.2	465	22 AAS6750	Human beta3 subun
23	21	1.7	1950	13 AAS2516	Villin gene promot
24	21	1.7	2352	22 AAK26255	Human immune/haem
25	21	1.7	11122	24 AAK04611	Human endoglycosu
26	21	1.6	658	22 AAK4296	Human foetal cDNA
27	20	1.6	2517	22 AAS1950	Mycobacterium tub
28	20	1.6	2517	22 AAS1950	Mycobacterium tub
29	20	1.6	2884	25 AAL55226	Wild-type bacteria
30	20	1.6	3325	22 AAL1660	Human immune/haem
31	20	1.6	4403765	22 AAK59683	Mycobacterium tub
32	30	1.6	4411529	22 AAI99682	Mycobacterium tub
33	30	1.6	4411529	22 AAI99682	Mycobacterium tub
34	30	1.5	471	22 ABA2213	Probe #679 for gen
35	19	1.5	471	22 ABA2213	Human bone marrow
36	19	1.5	471	22 ABA2213	Human bone marrow
37	19	1.5	471	22 ABA2213	Human bone marrow
38	19	1.5	471	22 ABA2213	Human bone marrow
39	19	1.5	471	22 ABA2213	Human bone marrow
40	19	1.5	471	22 ABA2213	Human bone marrow
41	19	1.5	471	22 ABA2213	Human bone marrow
42	19	1.5	471	22 ABA2213	Human bone marrow
43	19	1.5	471	22 ABA2213	Human bone marrow
44	19	1.5	471	22 ABA2213	Human bone marrow
45	19	1.5	471	22 ABA2213	Human bone marrow

ALIGNMENTS

RESULT 1
ID AAC67837 standard; cDNA, 1261 BP.

XX AAC67837;

DT 15-FEB-2001 (first entry)

XX Human beta3 cDNA.

XX Human; beta sub-unit; beta3; analgesic; anticonvulsant;

XX cerebroprotective; vasodilator; cardiac; nootropic; cytostatic;

XX desatolipid; gene therapy; beta3; analgesic; anticonvulsant;

XX familial nonchromaffin paraganglioma; phenylketonuria;

XX Charcot Marie Tooth disease; ss.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

P-PDB; ABB05689.

Human cDNA sequences and clones derived from human fetal brain, fetal kidney, melanoma, testis and amygdala cDNA libraries, useful in genetic screening and therapy -

Claim 1: Page 174-175; 61pp; English.

The present invention describes assemblies and computer readable media comprising novel human cDNA sequences and clones derived from human fetal brain, fetal kidney, melanoma, testis and amygdala cDNA libraries, useful in genetic screening and therapy. The present invention which encodes the proteins given in ABB0562 to ABB0575. The human cDNA sequences and clones can be used in gene therapy. The clones may be used in a variety of applications, for example, in the study of gene expression, for providing large arrays of human genetic material for implementing high throughput screening strategies and for treating diseases via gene therapy procedures.

Sequence 4052 BP; 994 A; 1033 C; 1036 G; 989 T; 9 other;

Query Match 87.5%; Score 1104; DB 24; Length 4052;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1254; Conservative 0; Mismatch 3; Indels 0; Gaps 0;

3 CTCCTCTCCAGCTGAGCTTACCTCTGGCGCAACACAGAGCGAGCGCGCTGCTGAA 62
Db 431 CTCCTCTCCAGCTGAGCTTACCTCTGGCGCAACACAGAGCGAGCGCGCTGCTGAA 490

Qy 63 GCTGAGCTTCCG 122
Db 491 GCTGAGCTTCCG 550

Qy 123 GCG 182
Db 551 GCG 610

Qy 183 CTCAGAGCG 242
Db 611 CTCAGAGCG 670

Qy 243 CTCCTCTCCAGCTGAGCTTACCTCTGGCGCAACACAGAGCGAGCGCGCTGCTGAA 302
Db 671 CTCCTCTCCAGCTGAGCTTACCTCTGGCGCAACACAGAGCGAGCGCGCTGCTGAA 730

Qy 303 AAGATCTGAGAGCG 362
Db 731 AAGATCTGAGAGCG 790

Qy 363 CAGCTCTCCAGAGCG 422
Db 791 CAGCTCTCCAGAGCG 850

Qy 423 CTCCTCTCCAGCTGAGCTTACCTCTGGCGCAACACAGAGCGAGCGCGCTGCTGAA 482
Db 851 CTCCTCTCCAGCTGAGCTTACCTCTGGCGCAACACAGAGCGAGCGCGCTGCTGAA 910

Qy 483 CAGCTCTCCAGAGCG 542
Db 911 CAGCTCTCCAGAGCG 970

Qy 543 CAGCTCTCCAGAGCG 602
Db 971 CAGCTCTCCAGAGCG 1030

Qy 603 CTCCTCTCCAGCTGAGCTTACCTCTGGCGCAACACAGAGCGAGCGCGCTGCTGAA 662
Db 1031 CTCCTCTCCAGCTGAGCTTACCTCTGGCGCAACACAGAGCGAGCGCGCTGCTGAA 1090

Qy 663 CAGCTCTCCAGAGCG 722
Db 1091 CAGCTCTCCAGAGCG 1150

Qy 723 CTCCTCTCCAGCTGAGCTTACCTCTGGCGCAACACAGAGCGAGCGCGCTGCTGAA 782
Db 1151 CTCCTCTCCAGCTGAGCTTACCTCTGGCGCAACACAGAGCGAGCGCGCTGCTGAA 1210

Qy 783 GAGCG 842
Db 1211 GAGCG 1270

Qy 843 CTCCTCTCCAGCTGAGCTTACCTCTGGCGCAACACAGAGCGAGCGCGCTGCTGAA 902
Db 1271 CTCCTCTCCAGCTGAGCTTACCTCTGGCGCAACACAGAGCGAGCGCGCTGCTGAA 1330

Qy 903 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 962
Db 1331 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1390

Qy 963 TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1022
Db 1391 TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1450

Qy 1023 GAGCG 1082
Db 1451 GAGCG 1510

Qy 1083 CAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1142
Db 1511 CAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1570

Qy 1143 CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1202
Db 1571 CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1630

Qy 1203 GTCTCTTACCTCTCATGAGCTTACGACACCTAAGAGCTCTCCAGACTGAGAGCGC 1259
Db 1631 GTCTCTTACCTCTCATGAGCTTACGACACCTAAGAGCTCTCCAGACTGAGAGCGC 1687

RESULT 3
AAB05689
ID AAB05689 standard; cDNA, 1510 BP.
XX AAB05689;
AC AAB05689; (first entry)
XX 07-SEP-2001
DE Human novel sodium channel beta-like subunit encoding cDNA.
XX Sodium channel, sensory neurons specific channel; beta-like subunit;
XX SNS; therapeutic; pain; analgesic; 99.
XX Homo sapiens.
XX Key Location/Qualifiers
XX CDS 213..860
XX /tag= a
XX /product= "sodium channel beta-like subunit"
XX NO200144293-A2.
XX 21-JUN-2001.
XX 14-DEC-2000; 2000W0-GB04802.
XX 17-DEC-1999; 99GB-0029970.
XX Plummer M, Powell AJ, Sansone P;
XX (GLAXO) GLAXO GROUP LTD.
XX WFT, 2001-398123/42.
XX P-PSDB; AAB05689.
XX Novel sub-unit for voltage-gated sodium channel proteins for producing


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Db 470 ACCACGCGTGTGAGATGCTTCTGACGCGCGGCGTGAAGATTCCTATTATTCAGG 529
Qy 604 TATGAGATGCTGCTGAGGTGTGAGAGGCTGCTGAGGCTGCTGAGGCTGCTGAGG 663
Db 604 TATGAGATGCTGCTGAGGTGTGAGAGGCTGCTGAGGCTGCTGAGGCTGCTGAGG 663
Db 530 TATGAGATGCTGCTGAGGTGTGAGAGGCTGCTGAGGCTGCTGAGGCTGCTGAGG 589
Qy 664 AGCAGGAGCTCTGAGGAGCTGCTGAGGCTGCTGAGGCTGCTGAGGCTGCTGAGG 723
Db 590 AGCAGGAGCTCTGAGGAGCTGCTGAGGCTGCTGAGGCTGCTGAGGCTGCTGAGG 649
Qy 724 CTCTACATCTGAGGTGCTGAGGCTGCTGAGGCTGCTGAGGCTGCTGAGGCTGCT 783
Db 650 CTCTACATCTGAGGTGCTGAGGCTGCTGAGGCTGCTGAGGCTGCTGAGGCTGCT 709
Qy 784 AGCAGGAGCTCTGAGGAGCTGCTGAGGCTGCTGAGGCTGCTGAGGCTGCTGAGG 843
Db 710 AGCAGGAGCTCTGAGGAGCTGCTGAGGCTGCTGAGGCTGCTGAGGCTGCTGAGG 769
Qy 844 GTCTCAGAAATCATGATGATACCTCTCTCTGCTCTCTCACCCTGTGGCTCTCAT 903
Db 707 GTCTCAGAAATCATGATGATACCTCTCTCTGCTCTCTCACCCTGTGGCTCTCAT 829
Qy 904 ATGATATTTATGTCATGAGAGCTCTCAAGAGCCGAGAGAGGACCCGAGAAAGCG 961
Db 830 ATGATATTTATGTCATGAGAGCTCTCAAGAGCCGAGAGAGGACCCGAGAAAGCG 887

RESULT 6
AAS86764
XX AAS86764 standard; cDNA, 1195 BP.
XX AC AAS86764;
XX AT 13-FEB-2002 (first entry)
XX DE DNA encoding novel human diagnostic protein #22568.
XX XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX OS Homo sapiens.
XX PA NC200175067-A2.
XX PD 11-OCT-2001.
XX XX 30-MAR-2001; 2001NC-US08631.
XX FR 31-MAR-2000; 2000US-0540217.
XX PR 23-AUG-2000; 2000US-0649167.
XX PA (HVS8-) HVS8Q INC.
XX PI Drmanan RT, Liu C, Tang YT;
XX XX WP1, 2001-639362/73.
XX PR P-F5DB; ABG23577.
XX XX New isolated polynucleotide and encoded polypeptides, useful in
XX forensic, chromosome mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity.
XX Claim 1: SEQ ID No 22568; 103pp; English.
XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes.
XX polypeptide chain reaction (PCR) primers, oligomers, and for chromosome
XX mapping. The polynucleotide (I) is also useful as a probe for
XX polynucleotides are also used in diagnostic and epidemiological
XX for identifying expressed genes. (I) is useful in gene therapy techniques
XX to restore normal activity of (II) or to treat disease states involving

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CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC sites expressing (II). (I) and (II) are useful for treating
CC sites expressing (II). (I) and (II) are useful for treating
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostic, forensic, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIFO
CC at ftp.wifo.in/pdb/published_pdb_sequences.
XX
XX Sequence 1195 BP; 253 A; 356 C; 381 G; 205 T; 0 other;
XX Query Match 31.4%, Score 396, BE 23, Length 1195;
XX Beef_Leuca Similarity 100%, 238-182;
XX Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy 490 AACCTCATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 549
Db 581 AACCTCATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 640
Qy 550 GTGTGCAATGTTCTCAGGCTCGAGGCGGTAAAGATTTCTTTTACAGATATCG 609
Db 641 GTGTGCAATGTTCTCAGGCTCGAGGCGGTAAAGATTTCTTTTACAGATATCG 700
Qy 610 AATGCGACAGAGGCTGAGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 669
Db 701 AATGCGACAGAGGCTGAGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 760
Qy 670 GACTCTCAGAGCTGCTCATCTGCTGCTCAAGCTCATCTGAGAGCTCTGCTCTAC 729
Db 761 GACTCTCAGAGCTGCTCATCTGCTGCTCAAGCTCATCTGAGAGCTCTGCTCTAC 820
Qy 730 ACTTCGATGTTCTCGGAGATTGAGTTGAGGCGCATCGCCCTTTGTGAAGAGCG 789
Db 821 ACTTCGATGTTCTCGGAGATTGAGTTGAGGCGCATCGCCCTTTGTGAAGAGCG 880
Qy 790 CGCTCATGCTGCTCGGAGATTGAGTTGAGGCGCATCGCCCTTTGTGAAGAGCG 849
Db 881 CGCTCATGCTGCTCGGAGATTGAGTTGAGGCGCATCGCCCTTTGTGAAGAGCG 940
Qy 850 GAATCATGATGATCATCTCTCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCT 885
Db 941 GAATCATGATGATCATCTCTCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCT 976

RESULT 7
AAS86763
XX AAS86763 standard; cDNA, 3531 BP.
XX AC AAS86763;
XX AT 13-FEB-2002 (first entry)
XX DE DNA encoding novel human diagnostic protein #22567.
XX XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX OS Homo sapiens.
XX PA NC200175067-A2.
XX PD 11-OCT-2001.
XX XX 30-MAR-2001; 2001NC-US08631.
XX FR 31-MAR-2000; 2000US-0540217.
XX PR 23-AUG-2000; 2000US-0649167.

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Query Match 17.3%; Score 218; DB 23; Length 621;

PR 22-AUG-2000; 2000US-0226279.
PR 18-AUG-2000; 2000US-0226279.

14-AUG-2000; 2000US-0225153.
18-AUG-2000; 2000US-0226279

14-AUG-2000; 2000US-0225153.
18-AUG-2000; 2000US-0226279

FILE REFERENCE: 2318-259
 CURRENT FILING DATE: 2000-03-23
 EARLIER APPLICATION NUMBER: U.S. 60/125,806
 EARLIER FILING DATE: 1999-03-23
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 44
 LENGTH: 713
 ORGANISM: Homo sapiens
 US-09-535-008-44

Query Match 1.4%; Score 18; DB 4; Length 713;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 191 CCACCGCGCTCCCAAGAC 210
 DB 256 CCACCGCGCTCCCAAGAC 273

RESULT 7
 US-09-252-991A-9940/c
 Sequence 9940; Application US/0925991A
 Patent No. 6551795
 GENERAL INFORMATION:
 APPLICANT: Marc J. Rubenfield et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 FILE REFERENCE: 107136.136
 CURRENT APPLICATION NUMBER: US/09/252.991A
 CURRENT FILING DATE: 1999-02-18
 PRIOR APPLICATION NUMBER: US 60/074,788
 PRIOR FILING DATE: 1998-02-18
 PRIOR APPLICATION NUMBER: US 60/094,190
 PRIOR FILING DATE: 1998-07-27
 SEQ ID NO 9940
 LENGTH: 933
 TYPE: DNA
 ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-9940

Query Match 1.4%; Score 18; DB 4; Length 933;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 323 CTTTCACCGCGGGAATCT 340
 DB 451 CTTTCACCGCGGGAATCT 434

RESULT 8
 US-09-252-991A-10137
 Sequence 10137; Application US/0925991A
 Patent No. 6551795
 GENERAL INFORMATION:
 APPLICANT: Marc J. Rubenfield et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 FILE REFERENCE: 107136.136
 CURRENT APPLICATION NUMBER: US/09/252.991A
 CURRENT FILING DATE: 1999-02-18
 PRIOR APPLICATION NUMBER: US 60/074,788
 PRIOR FILING DATE: 1998-02-18
 PRIOR APPLICATION NUMBER: US 60/094,190
 PRIOR FILING DATE: 1998-07-27
 SEQ ID NO 10137
 LENGTH: 1023
 TYPE: DNA
 ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-10137

Query Match 1.4%; Score 18; DB 4; Length 1023;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 323 CTTTCACCGCGGGAATCT 340
 DB 537 CTTTCACCGCGGGAATCT 554

RESULT 9
 US-09-023-942A-27/c
 Sequence 27; Application US/09023942A
 Patent No. 6479274
 GENERAL INFORMATION:
 APPLICANT: (US only) ANTLIS Toni Marie and HOOVER John David
 TITLE OF INVENTION: NUCLEIC ACID SEQUENCES
 NUMBER OF SEQUENCES: 30
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SCULLY, SCOTT, MORPHY & PRESSER
 ATTORNEYS/AGENTS: 10000 GARDEN CITY PLAZA
 CITY: GARDEN CITY
 STATE: NEW YORK
 COUNTRY: USA
 ZIP: 11530
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/023.942A
 CURRENT FILING DATE: 1998-02-18
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: P05101/97
 PRIOR FILING DATE: 1998-02-18
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PFO422/97
 FILING DATE: 18-NOV-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PFO422/97
 FILING DATE: 18-NOV-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: International PCT Application
 FILING DATE: 13-FEB-1998
 ATTORNEY/AGENT INFORMATION:
 ADDRESS: 10000 GARDEN CITY PLAZA
 REGISTRATION NUMBER: 11168
 REFERENCE/DOCKET NUMBER: 11168
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (516) 742-4343
 TELEFAX: (516) 742-4343
 TELEX: 230 901 SANS UR
 INFORMATION FOR SEQ ID NO: 27:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3846 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 ORIENTATION: 5' to 3'
 MOLECULAR TYPE: DNA
 US-09-023-942A-27

Query Match 1.4%; Score 18; DB 4; Length 3846;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 GTTCCCGCGCGGGAATCT 278
 DB 465 GTTCCCGCGCGGGAATCT 448

RESULT 10
 US-08-178-257-1
 Sequence 1; Application US/08178257

10-MAY-2001; 2001JU-0004922.
 (BION-3) BIONICS LTD.
 Mulley JC, Wallace RH, Scheffer IE,
 NPI; 2003-120544/11.
 N-PSDB; AB223837.
 New nucleic acid encoding a mutant mammalian beta-1 subunit of a
 voltage-gated sodium channel, useful for diagnosing e.g. epilepsy, or
 for screening modulators of sodium channel activity that may be
 employed for treating epilepsy.
 Claim 12; Page 47-49; 52pp; English.
 The invention relates to an isolated nucleic acid molecule (mutDNA) that
 encodes a mutant mammalian beta-1 subunit of a voltage-gated sodium
 channel, where a mutation event has occurred, which disrupts the
 functioning of an assembled sodium channel to produce an epilepsy
 phenotype. The mutation does not result in a C121W substitution in the
 beta-1 subunit, but in a mutation that results in a beta-1 subunit
 useful for diagnosing epilepsy, particularly generalized epilepsy with
 febrile seizures plus, or other disorders associated with sodium channel
 dysfunction. The polypeptide, polypeptide complex or genetically modified
 cell, or a pharmaceutical agent, or a pharmaceutical composition, or a
 technique) candidate pharmaceutical agent, particularly for modulators
 of sodium channel activity that may be employed for treating epilepsy or
 other disorders associated with sodium channel dysfunction. The selective
 molecule that is antisense or complementary to the mutDNA molecule is
 useful in the for treating epilepsy or other disorders associated with
 sodium channel dysfunction, or in the manufacture of a medicament for
 treating epilepsy or other disorders associated with sodium channel dysfunction.
 subunit of a human voltage-gated sodium channel.
 Sequence 218 AA;
 41.9%; Score 471; DB 24; Length 218;
 Best Local Similarity 49.5%; Gred. No. 3.3e-36;
 Matches 106; Conservative 31; Mismatches 69; Indels 8; Gaps 5;
 10 LASLVLYVYVCFVCPVPSVETAEVGNHMLKLCISCHGRFEVNTTVWVPSGG 69
 5 LALVQALVSSACCGCVGSVEATVYGMTKLCISCHGRFEVNTTVWVPSGG 64
 70 KQPL-1YEVNGHVEESP -FQRLGNQGS--KQLQVSTVLYVTLNDGLYTNQ 123
 65 BEFKILRYENHVLQLEDCFCFVNVGSGTGKQLQLSIFITVTVNHSUDYCHV 124
 124 REFTEFAHPPVKTILPLATVEAGDFTSVSVSTWILLVLTLLWLLMYCYRK 193
 125 RLFPFNYHNTSVYKTHIEYVDKANDNASIVSEIMVTLVLTLLWVAEMVICYK 184
 184 VKSA-TEAAGNSDYIALPSKENEN-SAYPVE 215
 185 IAAATETAGQENASEYLAITSSEKENTGVQVAE 218

Search completed: December 5, 2003, 23:18:29
 Job time : 82 secs